

# SEQUENCE LISTING

<110> Steinbuchel, Alexander  
Priefert, Horst  
Rabenhorst, Jurgen

<120> SYNTHETIC ENZYMES FOR THE PRODUCTION OF CONIFERYL  
ALCOHOL, CONIFERYLALDEHYDE, FERULIC ACID, VANILLIN AND  
VANILLIC ACID AND THEIR USE

<130> Bayer-9998-CAO

<140> 08/976,063

<141> 1997-11-21

<150> 196 49 655.1 GERMANY

<151> 1996-11-29

<160> 45

<170> PatentIn Ver. 2.1

<210> 1

<211> 32679

<212> DNA

<213> Pseudomonas sp.

<220>

<221> CDS

<222> (3146) .. (3997)

<223> gene = "ORF1"

<400> 1

```
gaattcatcc tcatggagca cttctacaag cagcaggcag gccaccctcc ccagaccgat 60
gacgtgcata ttatcgcgat cggcggaacg agctttaaac gctacctgga gctcggaaag 120
ctcctgaaca tcagagttgc cgcaattcga gataacgacg gtgactatca gcagaactgt 180
gtagcgaact acgaaggcta cctgtacgag tcggccaaga ttttcgccgc cccagatcct 240
gaccgaagca ctttcgaaat agggctgtac cgtgacaacc agaaagcctg tgacgatctc 300
tttgttgcgg gtcgcaaaaa actgaccgtg caagagtaca tgctcaaaaa taaagcggat 360
gccgctttcg agctgctgac caagaagtcc gctgaactga tcgccccgaa gtacatacag 420
gaagcgatcg aatggataag agcgtaattt tctccgtcgc aggatccggg aaaaccagcc 480
tgatcatcga gcgtctcagc cttgatcagc gggcattggt catcacttac acggacaaca 540
atcaccggca cctgcgcaac aggatcattc agagattcgg ggtgatccca tccaacatca 600
cgctcatgac gtaacttctcg ttcttgcatt gggttctgcta tcggcccttg atgcaattgc 660
agctaggaac acgaggccta aatttcagac gtccgcccaa caggcagtac cccctgaacg 720
```

atctcaatcg	gstatcgcgat	ggaagcggca	ggctctatca	ctgcgcctc	gcgaaactgc	780
tggacgttgc	gcaggcctta	cgggatgtgc	gtgcccgcct	ggagcgcttt	tacgactgcc	840
tgtacgtcga	cgaggtacag	gatttcgcgg	gtcacgactt	caacctcctg	ctggagggttt	900
cacgggcgaa	gatcggcatg	acgttcgtcg	gtgatttcca	ccagcacacc	ttcgatacca	960
gccgagacgg	agcggtaaac	aaaacccttc	acgacgatgc	cgttcgctac	gagaagcgct	1020
ttcgtgatgc	cggcatttcg	gtggacaagc	aaacgttgaa	cgcagctgg	cgatgcgcca	1080
aaacggtctg	tgacttcatc	agcgcaaaagc	tgaaaattgg	cgatggacgc	tcacgaggag	1140
cggggcagcc	ggatcattag	agttgatgac	caagagcagg	ccaacttggt	gcacgttgac	1200
ccaaccatcg	tgaagctggt	tttgagcgaa	cactacaagt	acggctgcca	ctccgaaaac	1260
tggggggcaa	gcaaggcatg	gatcacttta	acgatgtctg	cgttgtgatg	ggcccgggta	1320
tctggaaaga	ctatgtggct	gagaggttac	accaggccaa	cccgcaaacc	cgaaacaagc	1380
tgtacgtggc	ctgcactagg	gcgcggggtg	atctgtattt	cgtgcctgag	aagctcttga	1440
gggccttcaa	acagggaaat	taggcgataa	agctgaaaaa	ggattttcaa	gtaaagacca	1500
ctccttcctt	actcgatgtc	cgcttttggc	cgattttctgc	cagtcacgac	cggcaaagaa	1560
cggccaaaag	cggactgatg	cggttactaa	gcctgcctct	tattgaagct	tggtgggctt	1620
taagaatgtg	gtgcgatcca	gcctgatgat	gttccgcttt	atgcacgcag	ccaagcctat	1680
cgaccgccgt	ctgcacgttg	taaccgacta	cgctgtgcc	tttgccgctg	gtggccatgg	1740
agcgtgcatc	cggatcggtg	agtgagactt	gcccattccg	tgcttcacgt	agctgctgct	1800
ccatctcctt	gagcgcctgc	atctgctggc	ggagtttctc	gattttatcc	tggaggcggc	1860
tggctttggc	ttcggcgaca	toggattgag	ttctgtcggc	ggtgtccatc	gctgccagat	1920
agcggtcgat	gattttatca	atctggtcca	tccgggcgcg	caccgcctat	gatccggagt	1980
cctccgatat	cgatgaggcc	tatctgggct	ggaagagcgg	ttcgggtgtc	tcagaccttg	2040
gcgagaacgc	ggtcaagctc	agcttcgggc	gccaagcctt	caagatcggc	aacggcttcc	2100
tgatcggcga	aggccacgtc	gaccaaggta	acgatgcggg	ctactggctg	gcccctacct	2160
aggcgttcga	caacaccgtc	ctagcccaac	tggacaccgg	caagctgcat	gtcgacctgt	2220
tcgacctcca	ggcgggcatg	gatctggacg	tcgccgacat	caaggagaaa	gtccgggtgc	2280
gcgggggcaa	cgtcgagtgg	cgcgacgaga	cctacggcac	ggtagggttc	accggcttcc	2340
atacgttgga	cgctgacaat	cogctgcgcg	acggcatgaa	tgtctacgac	gtacgcgcat	2400
cgggcagccc	gatccgagcc	ctgcgcgagg	tggccctggc	ggcggagtac	gcctggcagc	2460

gcggcggcgca	ggcggacaag	acgagtgagg	cctggtacct	acagggcagc	tacacctttc	2520										
gggatgcccc	ctggacgcca	gtgctgatgt	accgtcacgc	ggtctttctc	gacgactacg	2580										
actccctgct	gtacggctaa	gggggcaaca	acatgggctg	gaaaggagca	ttgcgttgaa	2640										
acgatgctga	agggcgtcac	tcttttactg	ctgtccgctc	acgtcgaaac	tgcattgattt	2700										
cgggcagcct	ttcttctatc	cagtcggcca	gcacctgaac	atgagccgct	acttcctggc	2760										
caagcggcgt	caggctgtac	tcgacatgtg	ggggaacgac	cgggagcgaa	tgtcgagcta	2820										
tgaaaccgtc	tccctccagg	ccttgtaggg	tctgcgcaag	cattcttttc	gctgacaccg	2880										
ccgattcttc	cgacgcaggt	cgctgaatcg	atggacaccg	tccaccaaga	tgatcagcac	2940										
gagcacgccc	agcggcttgt	cacgtgcttg	agcacgtccc	gcgacggcat	tcagcactca	3000										
gcaattcccc	cgccgtgctt	gcatggagag	actggtaagg	gcggccagcg	tgagtttcat	3060										
ggcactaacc	tttatgtatg	tacttacttt	tagttgctag	tagggatatg	gtgacgcctt	3120										
catcctacga	aacaagtgaa	gactg	atg	atc	gcc	atc	aca	ggt	gcc	tcc	gga	3172				
			Met	Ile	Ala	Ile	Thr	Gly	Ala	Ser	Gly					
			1					5								
caa	ctt	ggt	cgg	ttg	act	ata	gag	gcg	cta	ctg	aag	cgc	ctg	cca	gca	3220
Gln	Leu	Gly	Arg	Leu	Thr	Ile	Glu	Ala	Leu	Leu	Lys	Arg	Leu	Pro	Ala	
10					15				20					25		
tcc	gaa	att	att	gcc	ctc	gtc	cgg	gat	ccg	aat	aag	gcc	gga	gac	ctt	3268
Ser	Glu	Ile	Ile	Ala	Leu	Val	Arg	Asp	Pro	Asn	Lys	Ala	Gly	Asp	Leu	
				30					35					40		
acc	gca	cgt	ggc	atc	gtg	gtg	cgc	cag	gcc	gat	tac	aac	cgg	ccg	gaa	3316
Thr	Ala	Arg	Gly	Ile	Val	Val	Arg	Gln	Ala	Asp	Tyr	Asn	Arg	Pro	Glu	
			45					50					55			
aca	ctc	cac	cgg	gcc	ctg	att	ggg	gtc	aac	cgg	ttg	ctg	ttg	att	tcc	3364
Thr	Leu	His	Arg	Ala	Leu	Ile	Gly	Val	Asn	Arg	Leu	Leu	Leu	Ile	Ser	
		60					65					70				
tcc	agt	gag	gtg	ggt	caa	cga	act	gcg	caa	cac	cgg	gca	gtg	atc	gac	3412
Ser	Ser	Glu	Val	Gly	Gln	Arg	Thr	Ala	Gln	His	Arg	Ala	Val	Ile	Asp	
	75					80					85					
gct	gcg	aag	caa	gaa	ggt	atc	gag	ttg	ctg	gct	tat	acg	agt	ctg	ctt	3460
Ala	Ala	Lys	Gln	Glu	Gly	Ile	Glu	Leu	Leu	Ala	Tyr	Thr	Ser	Leu	Leu	
90					95				100					105		
cat	gcc	gat	aaa	tcg	gcg	ctg	ggc	cta	gcg	act	gaa	cac	cga	gac	acg	3508
His	Ala	Asp	Lys	Ser	Ala	Leu	Gly	Leu	Ala	Thr	Glu	His	Arg	Asp	Thr	
				110				115						120		

gaa	cag	gcc	ctg	aca	gag	tcc	ggg	att	cct	cat	gtc	ctg	ttg	cgc	aac		3556			
Glu	Gln	Ala	Leu	Thr	Glu	Ser	Gly	Ile	Pro	His	Val	Leu	Leu	Arg	Asn					
			125					130					135							
ggg	tgg	tat	cac	gag	aac	tac	acg	gcg	ggc	atc	cca	gtc	gcg	ctg	gtt		3604			
Gly	Trp	Tyr	His	Glu	Asn	Tyr	Thr	Ala	Gly	Ile	Pro	Val	Ala	Leu	Val					
			140				145					150								
cat	ggc	gtg	ttg	ctg	ggc	tgt	gcc	cag	gat	ggc	ttg	att	gct	tct	gct		3652			
His	Gly	Val	Leu	Leu	Gly	Cys	Ala	Gln	Asp	Gly	Leu	Ile	Ala	Ser	Ala					
			155			160					165									
gca	cgt	gct	gac	tac	gcc	gaa	gca	gcg	gct	gtg	gtg	ctc	acc	ggg	gag		3700			
Ala	Arg	Ala	Asp	Tyr	Ala	Glu	Ala	Ala	Ala	Val	Val	Leu	Thr	Gly	Glu					
170					175					180					185					
aat	cag	gca	ggg	cgc	gtc	tac	gag	ctg	gcc	ggg	gaa	ccg	gca	tat	acg		3748			
Asn	Gln	Ala	Gly	Arg	Val	Tyr	Glu	Leu	Ala	Gly	Glu	Pro	Ala	Tyr	Thr					
				190					195					200						
ctc	acc	gaa	ctg	gca	gct	gag	gtg	gcg	ccg	caa	gca	gga	aag	acc	gtc		3796			
Leu	Thr	Glu	Leu	Ala	Ala	Glu	Val	Ala	Pro	Gln	Ala	Gly	Lys	Thr	Val					
			205					210					215							
gtg	tat	tcg	aac	cta	tcc	gag	agc	gat	tac	cga	tct	gcg	ttg	atc	agt		3844			
Val	Tyr	Ser	Asn	Leu	Ser	Glu	Ser	Asp	Tyr	Arg	Ser	Ala	Leu	Ile	Ser					
			220				225					230								
gcg	ggc	ctt	ccc	gat	ggg	ttt	gcg	gca	ttg	ctc	gca	gac	tct	gat	gca		3892			
Ala	Gly	Leu	Pro	Asp	Gly	Phe	Ala	Ala	Leu	Leu	Ala	Asp	Ser	Asp	Ala					
			235			240					245									
ggc	gca	gcc	aag	ggg	tat	ttg	ttt	gat	tcc	agt	gga	gac	agt	cgc	aag		3940			
Gly	Ala	Ala	Lys	Gly	Tyr	Leu	Phe	Asp	Ser	Ser	Gly	Asp	Ser	Arg	Lys					
250					255					260					265					
ctg	atc	ggg	cgc	cca	acc	act	ccg	atg	tcg	gaa	gcc	atc	gcg	gca	gca		3988			
Leu	Ile	Gly	Arg	Pro	Thr	Thr	Pro	Met	Ser	Glu	Ala	Ile	Ala	Ala	Ala					
				270				275						280						
att	ggc	cgc	taaaaactgca ttttcgcgcac ttgagtgaca cctggggttag													4037				
Ile	Gly	Arg																		
ata	acc	cagg	tgt	cgc	cac	cgc	ttt	gggt	tag	ggg	ggg	caat	agc	ggg	gtc	tggtcac	4097			
cgc	ttg	cccc	gcg	gcgcgc	cgc	cgc	tatt	tgga	tgatt	ctc	caa	ctt	cct							

gtcttcgctg acataacctt tctcaaatag ggcacgccc tgggccaagc actgcaagag 4517  
gatctcttgc gtttcaactg atagccctcg ctccgcagcc tgccttgagg ccagtccttc 4577  
aagtaccctt cgaacctcca ccgcgcctgc caggtcattt ggggtcattt gccgcactgc 4637  
atagccacgt gcgccttggc gatcagtaac ccttcctggt ctacgcctcg gaacgcaatg 4697  
cggatagggtg tgcgcgcaca ctcccaggcg ctccgcagtg gggatttcgg cgatgcgctc 4757  
tcctgcccgg agttcgccat ccacaatcat tttgcgcagt agattgagta ctccgtgccc 4817  
gggcccgcct atttcagcct ccgattggat ccagtaatgg tttgagagaa ttttactcgc 4877  
aagggtattt tgggcaatag ccccgctgat tgctggtttt tgtatgtggc gtgcgactat 4937  
cgcacagaat tggatccacc ttggcgcaaa aaaactggag ctacctcatc ggtcgtgggt 4997  
atattggatc ccataaggtc aagttcatag ctgatttttg ctttagatgt ccattgtgga 5057  
tccaaaaaca agatcgccat tgaggaacgc gccatgtttc cgaaaaacgc ctggtatgtc 5117  
gcttgacttc cggatgaaat cgcagataag ccgctaggcc gtcagatctg caacgaaaag 5177  
attgtcttct atcggggggc ggaaggacgt gttgccgcgg tagaggattt ctgccctcat 5237  
cgcggggcac cgttgtccct gggtttcggt cgcgacggta agctgatttg cggctaccac 5297  
ggtttgaaa tgggctgcga gggcaaaacg ctccgcagtc ccgggcagcg cgttcaaggc 5357  
ttcccttgca tcaaaagcta cgcggtagaa gagcgatacg gctttatctg ggtatggcct 5417  
ggtgatcgcg agctggcgga tccggcgctt attcaccacc tggagtgggc cgataatccg 5477  
gagtgggcct atgggtggcg tctctaccac atcgtttgtg attaccgcct gatgatcgac 5537  
aacctcatgg atctcaccca tgagacctat gtgcagcct ccagcatcg tcaaaaggaa 5597  
attgacgagg caccggtcag tactcgtgtc gagggcgaca ccgtgattac cagccggtac 5657  
atggataacg tcatggcccc tccgtttctg cgtgctgcgc ttcgtggcaa cggcttggcc 5717  
gacgatgtac cggttgatcg ctggcagatc tgccgattcg ctctccgag tcacgtactg 5777  
atcgaagtag gtgtgggtca tgcgggcaaa ggcggatatg acgcgccggc ggaatacaag 5837  
gccggcagca tagtggtcga cttcatcacg ccggagagtg atacctcgat ttggtacttc 5897  
tggggcatgg ctccgcaact ccgtccgcag ggcacggagc tgactgaaac cattcgtggt 5957  
ggtcagggca agatttttgc cgaggacctg gacatgctgg agcagcagca gcgcaatctg 6017  
ctggcctacc cggagcgcca gttgctcaag ctgaatatcg atgccggcg ggttcagtca 6077  
cggcgctca ttgatcggat tctcgcagct gaacaagagg ccgcagacgc agcgtgatc 6137  
gcgagaagtg catcatgatt gaggtaatca tttcggcgat gcgcttggtt gctcaggaca 6197

**T**

1

ggccatcttc ggcctgggcg gcatcggett ggcgggcgatc atcgggcgga agatggccaa 7937  
ggcctcgcg atcatcgcca tcgacatcaa tccgtccaag ttcgatgtgg ctcgcgagct 7997  
ggcgccact gacttcgtca atccgaacga tcacgcgaag ccgatccagg atgtcatcgt 8057  
cgagatgact gatggcggtg tggactacag cttcgagtgc atcggaacg ttcgactcat 8117  
gcgcgagca ctcgagtgt gccacaagg ctggggcgaa tccgtgatca tcggcggtggc 8177  
gccggcgggg gccgaaatca acaccgtcc gttccacctg gtgaccggtc gcgtctggcg 8237  
gggttcggcg ttcggtggcg taaagggcc caccgaactg ccgagctacg tggagaaggc 8297  
acagcagggc gagatccgc tggacacctt catcactcac accatgggcc tggacgacat 8357  
caacacggcc ttcgacctga tggacgaagg gaagagcatc cgctctgttg ttcaattgag 8417  
tcgctagtga agtggggtga ggaaattgga ttaggaggcg gatggttcct gccgcttaac 8477  
caccttgtcc cagcttctgg ctgagatttc caagattcgg tgaaatttgc catgccgcaa 8537  
actcttgctg gacggttgag tctgttatcc ggcaccgacg aattaaccct gcttcttcgg 8597  
ggtggtcggg gcattgagcg tgaagccttg cgggtcgatg ttcaaggtga actggcgctg 8657  
acgcctcacc cggcgcgct tggctctgcg ttgaccatc cgacaattac tacggattac 8717  
gccgaggccc tgcttgagtt gatcactcgg ccggcaaccg attgtgcga agccttggt 8777  
gagctggagg agcttcaccg tttcgttcat tcgagacttg agggggagta tctctggaat 8837  
ctgtccatgc ctggcagatt gccggttgat gagcaaatcc cgattgcttg gtatggacca 8897  
tcaaatccag gcatgttgcg ccacgtttat cgccgtggcc tagctctgcg ttatggcaag 8957  
cgaatgcaat gcatcgcagg gattcactac aactactcac tgccgccaga gcttttcgct 9017  
gtcctgacca aggcagaggt cgggtctccc aagttactgg agcgccagtc agcagcttac 9077  
atgcgccaaa ttcgcaacct tcggcaatac gggttggtgc tggcctactt gttcggcgct 9137  
tccccgcca tctgcaagag cttcttgggg ggcgagagag atgagctagc tcgcatgggg 9197  
ggcgatacgc ttacatgcc ctatgcaacc agcttgcgca tgagtgacat cgggtaccgc 9257  
aaccgtgcca tggatgatct atctcccagc ctgaatgac tgggtgccta tattcgcgat 9317  
atgtgccgtg ctcttcacac tcccgatgcc cagtaccagg cgctgggtgt gtttgcacag 9377  
ggcgagtggc ggcagttaaa cgccaatcta ttgcagttgg atagttagta ctacgcactg 9437  
gcgcgaccga agtcagcgcc cgagcgggg gagcgaaacc tggatgctct cgctaggcgt 9497  
ggagtccagt atgtggagct gcgcgcactg gatctcgatc cattctcccc gttaggcatt 9557  
ggcctgacct gcgccaagtt cctcgatggc tttttgcttt tctgcttggt gtctgaggcg 9617

ccggttgatg atcgaaatgc ccagcgttca agaccgggaa aatctgagcc tggccggcaa 9677  
 gtacgggctg cacctggctt aaagctgcat cggaatggtc agtccattct cctcaaggat 9737  
 tgggctgagg aagtgttgac ggaggttcag gcctgtgtgg aattgctcga cagtgcaa 9797  
 gggggctcat ctacgcatt ggcttggtca gcacaggagg aaaagggtgct taatccgat 9857  
 tgtgcgccat cagctcagg gctcgcagag atacacagac acgggtgggag cttcacggca 9917  
 tttggctgcc aattagctat cgaccatgca aaacacttca gtgcctcctc gcttgaggct 9977  
 ggcgtagcca aagcgttga cctccaggcg acgtcgtctc tgcgcgagca gcatcaattg 10037  
 gagggcaacg accgtgcgcc attttctgac taccttcagc aattctccct ggctttcggg 10097  
 caatccgtcg gcgcctctcg tgcgccaac cctaccgcgc acctcatcga tctgaccct 10157  
 cctgtctaag gttgtcgtgg gagcagatcc gtgggcccag cttcctccag ggctggccg 10217  
 cagcgatcca gttgctaggt ccctatgctc ttgcataggg taaaaattag ttattgtgtt 10277  
 taacgaaacg tctggcatac tggctttagg cacgagcttc cacgccgaag ttgagagcgt 10337  
 catgaacgat ttttctgtg gagagacgat gcccgatgag gtcgacgagg ttcaggctct 10397  
 aatggcagtg ccggcggcta aacggaacgt gccgtatttt gaggcttgga gcgtggtgaa 10457  
 gcagcttggc tgctccctgg gcctgtcagg atcacgctgt gtcggcagtg acacttcaaa 10517  
 acaagaaggg cattaagatg atgaatgtta attataaggc tgcggggcg agcctactcc 10577  
 tcgccttcat ctctcaggga gcttgggcag agagccccgc agcctctggc aatacccctg 10637  
 acatttatcg aaagacctgc acctactgcc atgagcctac tgtcaacaat ggccgggtca 10697  
 ttgccgaag cctcgggccc actctgcgag ggcgccagat cctccacag tacacggagt 10757  
 acatggtgag tcatggacgc ggggcaatgc ctgcattctc tgaagcagaa gtgcctccg 10817  
 cggagctgaa agttctgggc gattggattc agcaaagcag tgctcccaa gacgctggag 10877  
 tcgcgccatg actaccgctc gcaactttct aataggcgcg tcgcagggtg gggcattggt 10937  
 gatgatgtcg ccgaaattgg tcttccgtac gccgctcaag cagaagcccg tgcgcacct 10997  
 gtcgaccggg ctggccgggt agcaagagtt tctcgcagtg cttcgcgcgc gattgacca 11057  
 tacgggtcag gtcgacatcg cgtcggtacc gctggacgca gctatttggg cttctccgc 11117  
 tcgacttgcc caggcaatgg atgcgttgaa tggtagcgt ctgacgctt ttgttgagcc 11177  
 caggaacgaa ttgatactga tgcaattctt gatggatcgc ggggctgcgg tgcttattca 11237  
 aggtgagcat gcggtggaca gcaagggggg ctctcggcac gactttctga gtacccatc 11297



cagtgcggga attggagggg cgctagccga cagcctggca aaagggggct cgccgttctc 11357  
 tatttccgtc cgagcgcttg gctcggtaac tgctcagcca agaagtaatc agagtgaggt 11417  
 ggccaccac tggacgaccg ctctggggac ctattatgcc gatatcgagc tggggcgctg 11477  
 ggagccgcag cgcaagtgg ccagctatgg aagtggacta atcatggcgg aacggcttga 11537  
 tcgtgttgcc tcaaccttca ttgcagatct ctgagtcagg gtattgatat ggaaagcacc 11597  
 gtagttcttc ccgaggggtgt caccocggag cagttcacca aagccatcag cgagttccgt 11657  
 caggatttgg gtgaggacag tgttcttgct actgctgaac gagttgttcc ctatacga 11717  
 ctctcattc ctacacagga tgatgcccag tacaccccg cgggtgcctt gactccttct 11777  
 tcggtggagc aggtccagaa agtcatgggg atctgcaata agtacaagat cccggtatgg 11837  
 ccaatctcta ccggtcggaa ctgggggtat ggggtccgctt cgcctgcaac tcctgggcag 11897  
 atgattcttg accttcgcaa gatgaacaag atcattgaga tcgatgttga ggggtgtact 11957  
 gccctgctcg agccgggctg tacctaccag cagcttcacg attacatcaa ggagcacaat 12017  
 ctgcccttga tgctggatgt gccgactatt gggcctatgg ttggcccggg gggtaacacg 12077  
 ctggatcgag gcgttggtta tacgccgtac ggcgagcact tcatgatgca gtgtgggatg 12137  
 gaagtcgtca tggccgatgg cgaaatcctc cgtactggta tgggctcggg gcccaaagcc 12197  
 aagacttggc aggcattcaa atggggctat ggtccatata tggacggtat ctttaccag 12257  
 tccaactttg gtgttggtac aaagctcggg atttggttga tgcccaagcc gccagtgatc 12317  
 aagtcgttta tgatccgta tccaatgaa gctgatgtgg ttaaggcaat tgatgctttt 12377  
 cgcccgctgc gtattactca gctgattcct aacgtcgttt tgttcatgca cggcatgtac 12437  
 gaaacggcaa tctgccggac gcgtgctgag gttacttcgg acccaggtcc tatttctgaa 12497  
 gcggacgcc gcaaagcatt caaagagcta ggcgttggt actggaacgt ttacttcgcg 12557  
 ctttacggca cagaagagca gatagccgtc aatgaaaaga tcgtccgcgg catcctcgaa 12617  
 ccgacggggg gtgagatcct caccgaagag gaggctggag ataacattct tttccatcac 12677  
 cataagcagc tcatgaacgg cgagatgaca ttggaggaaa tgaatatcta ccagtggcgc 12737  
 ggagcaggtg gcggtgcttg ctggtttgca ccggttgctc aggtcaaggg gcatgaggca 12797  
 gagcagcagg tcaagcttgc tcagaaggtg cttgcaaagc atgggttcga ttacacggcg 12857  
 ggctttgcga ttggttggcg cgatcttcac catgtgatcg atgtgctgta cgaccgtagc 12917  
 aatgccgacg agaaaaagcg cgcttacgct tgctttgatg aattgatoga cgtctttgcg 12977  
 gccgaaggct ttgcaagtta caggaccaat attgccttta tggacaaagt cgctctaag 13037

ctcggcgctg	agaataagag	ggtcaatcag	aagatcaagg	ctgcccttga	tccaaacggc	13097
atcatcgctc	cgggcaagtc	gggcattcat	cttcccaaat	aatgcgtggt	cgtgaggcgg	13157
ctgctagccg	cctcatttga	agaaagagtc	gtatcggcga	tgcatgatgc	gtcgttcgct	13217
ctcggctggt	gattcttcga	aagaagcgta	tgggggggga	atgattgcaa	tactgcggg	13277
caccggaagt	cttggtcggg	ctatcgttga	gcgactaggg	gactgcggtc	ttatcggtca	13337
agttcgattg	acggctcgcg	atcctaaaag	gcttcgtgcc	gctgccgagg	aagggtttca	13397
ggtcgctaag	gcggattacg	ccgatattgg	gagtcttgac	caggcattac	agggggtaga	13457
cgtattactc	ctgatttctg	gtactgcacc	caatgaaata	aggatccaac	agcataagtc	13517
ggtcatcgac	gcggcaaaac	gaaacggcgt	gtcgcgtatt	gtgtatacca	gcttcataaa	13577
tccaagtact	cgcagcaggt	ctatttgggc	ctccattcat	cgtgaaactg	agacttacct	13637
caggcagttc	gggggtgaagt	ttacgattgt	ccgaaataat	cagtatgcgt	ctaacctgga	13697
tctgttgctg	ctgagggctc	aagacagcgg	aatatttgcc	attcccgggg	cgaagggggc	13757
ggtggcgta	gtctctcatc	gcgacgttgc	cgctgccatc	tgtagtgtcc	tgacgaccgc	13817
cggacacgat	aacaggatct	accagctcac	aggctctgag	gctctcaatg	ggctcgagat	13877
cgcggagatt	cttggtgggg	tgctcggggc	tccagtgcgc	gcgatggatg	cctcgccctga	13937
cgagtttgct	gccagctttc	gcgaggctgg	attccctgag	tttatggttg	aaggcctact	13997
aagcatthtat	gccgcttcag	gtgctgggga	gtaccaatcc	gtcagtcctg	atggtgggtt	14057
gttgacggga	cgacgtgccg	aatcgatgcg	aacttacata	cagcgtctag	tttggccttg	14117
agggaggtga	ccgacgtatg	aaggcttatg	agcttcacaa	gatttcggaa	caggtagagg	14177
tcaggctcca	gccaaactcg	ccccgcccgc	agttgaatca	tggcgaggtc	ctcatcaggg	14237
tccatgcagc	ctcgtctaac	tttcgcgatt	tgatgatctt	ggccggctgc	tatccgggtc	14297
aaatgaaacc	cgatgtgata	ccgctgtccg	atggtgctgg	cgagattgtg	gaggtcgggc	14357
ctggcgatat	ttcggaggtg	cagggtcagc	gcgtagccag	cacctttttc	cctaactggc	14417
gggccggaaa	gattaccgag	cgggctattg	aggtgtcggt	gggcttcggg	atggacggga	14477
tgctcgcgga	atacgttgct	ctgccctatg	aggcaacgat	accgataccg	gagcacctgt	14537
cgtacgagga	ggctgcaaca	ttgccttgcg	cggcgctaac	cgcttggaat	gcgttgaccg	14597
aagtggggcg	tgtcaaggcc	ggtgatacgg	tcttgttgct	tggcactggc	ggtgtctcga	14657
tgttcgcgtt	gcagttcgcc	aagctcttgg	gggcgacggt	cattcacacc	tcgagcagtg	14717

aacaaaaagct	ggagaggggtg	aaagcgatgg	gggctgatca	tctgatcaac	taccgcaatt	14777
cgccaggggtg	ggaccgtact	gtcctggatc	tcaccgcggg	gcgagggggtt	gacctggtag	14837
tcgaggtagg	gggggcgggg	accttggagc	gctcacttcg	tgcggtcaag	gtaggcggtg	14897
ttgtcgccac	gattggggcta	gtggctggcg	ttggccccgat	tgaccattg	ccgcttatct	14957
ccagggctat	tcagctctcg	ggcgtctatg	tcggttcccc	ggaaatgttt	ctctcaatga	15017
acaaagccat	tgcatacagc	gaaatcaagc	cagtgatcga	ttgctgcttc	cccatcgacg	15077
aggttggaga	tgcttatgag	tacatgcgta	gcggcaatca	ccttggcaaa	gtagttatca	15137
cgatctaact	gccgctaaac	ccgttgtgcg	gcaatttgcg	ggagctagta	ccgggctttc	15197
ggtttggctc	ttggatggtc	ttcgcatgca	cgctttacga	agggggccag	ggacagacgc	15257
cccggggcgt	aatcaatggc	cttgcgtgca	ggctctcacc	gtcgtgatcg	ggattggaaa	15317
ttcgtgcgag	gacagcggcc	acgtaccggc	gccctgaagg	gctggaaggt	tggagtttcg	15377
ttaaggtctg	gtaccacgca	gccatggaga	gcggccctta	gccggaatgg	cagcttgatg	15437
gttgccacgg	gaccagactg	gatgtcttga	gtgtcgagaa	ttaccagatc	gctgcgattt	15497
tcatacgaggc	gaccaaccac	ggtcagcaag	taccgcgcac	cttcggcggc	ggtcggactt	15557
ctagggacga	aggccggctc	ctggggccgc	gaggcttcgc	cggagtacca	gaggtcgtag	15617
tcacctcggt	ggttgtccca	gatgccgagt	gagttgtacg	cgaatatctt	ctcggcctgc	15677
tgatgcgcaa	gtggtttgcg	tggatcgtcc	acccccataa	agccatagcg	gttgcatthc	15737
agggcgaacg	aagaatccat	gattggcatt	tccgcaaaga	aatcgtgtag	ccgggttcgc	15797
ttgatctcgt	cgctgctgct	atcgaggcca	atttcccaac	gagtcaggcg	tggtacggct	15857
ttctcagggg	cgaaggggtg	gttttgtgag	ttgggggaagg	ggaacggcag	gatttcactt	15917
tccataaggt	cgatataaat	cttgggttcg	acttcccaag	cattcacaac	atgaaatacc	15977
cagagcgccg	gtgccttgag	ccagcgaatc	agactgccct	ggcgcggcgc	gagtacgcca	16037
atgtagctgc	ccagttccgg	ctccacata	taaattggct	gtttcgccct	gaggcgggac	16097
aggctgttgg	tggccggcat	aattgggaaa	atggaccaat	ttcgggtaat	ggcaaagtcg	16157
tgcataaatg	cgccataggg	ctgctcaaac	caagtttcat	gtgtcacctt	gccgtgcttg	16217
tcgacaatgt	aataggccat	gtctggagtt	gcttcgccct	tagctgccga	accgaagaac	16277
aacaagtcac	ccgtttccgg	gtcatatttt	ggatgggcgg	tgtggggttg	gctggtaact	16337
tggccgtcgt	agtcgaagtg	tccgcgagtt	tcaagtgtac	gaggatccag	ttcgtacggg	16397
aggccgtctt	ccttcaccgc	cagcaccttg	ccgtgatggc	taatgatgct	tgtattggca	16457

acggtgcggt	ctagtccttt	tacactgggtg	tcgtcgggtat	aggggtttct	gtacatgcca	16517
aatagcgatt	ttcgcgctag	tcgttcggcc	gtgaatcgag	cggttttaac	ccagcgactg	16577
atgaatcgca	catgaccatc	ttcgaagtgg	aaggcagagg	ccattccatc	tccatctatg	16637
aaggtgtgga	atTTTTgtgg	ggtaacttga	ggctctggcg	tattacggta	gaacgttcca	16697
tttattgatt	ttgggatttc	gccgtcaacc	tctagatcga	acaagtctgc	ctctatacgg	16757
gtggggagaa	gtgttcctac	taattgcggg	tcgttgcggt	tgaatctcgc	catggcacgg	16817
tctcctttgt	tgttctgaat	ggcctaaatg	cgcggtctgc	cgggttgag	tttatgttta	16877
ggactgaccg	gatttcatgt	gtgccgggtga	agtgaagatg	tctgtgagtg	caatggtggt	16937
ggtattgaaa	atggggccgag	gctggcctat	tgtttagaat	ttcaagaatg	acaactattc	16997
ggtggcgcg	tatgtccatt	cactctgagg	ggatcactct	cgcggattcg	ccgtgcatt	17057
gggcgcatac	cctgaatgga	tcaatgcgta	ctcatttcga	agtccagcgt	cttgagcggg	17117
gtagagggtgc	ctcccttgcc	cgatctagat	ttggcgcggg	tgagctgtac	agtgccattg	17177
caccaagcca	ggtacttcgc	cacttcaacg	accagcgaaa	tgctgatgag	gctgagcaca	17237
gctatttgat	tcagatacga	agtggcgctt	tgggcgttgc	atccggcgga	agaaagggtga	17297
tcttgggaaa	tggtgattgc	tccatagttg	atagtcgcc	agacttcaca	ctttcctcga	17357
actcttcgac	ccaagggtgc	gtaatacgct	ttccgggtgag	ttggctggga	gcgtgggtgt	17417
ccaatccgga	ggatcttatac	gcccgcgag	ttgatgctga	ggtaggggtg	ggtagggcgc	17477
taagcgcatac	ggttttctaat	ctagatccat	tgcgcatacga	cgatttaggt	agcaatgtaa	17537
atggcattgc	agagcatggt	gctatgttaa	tttactagc	aagtctctgcg	gttagttctg	17597
aagatggggg	tgtggctctt	cggaaaatga	gggaagtga	gagagtactc	gagcagagtt	17657
tcgcagacgc	taatctcggg	cgggaaagtg	tttcaagtca	attaggaatt	tcgaaacgct	17717
atttgcatta	tgtctttgct	gcgtgcggta	cgacctttgg	tcgcgagctg	ttggaaatac	17777
gcctgggcaa	agcttatcga	atgctctgtg	cggcgagtga	ctcgggtgct	gtgctgaagg	17837
tggccatgtc	ctcaggtttt	tcggattcaa	gccatttcag	caagaaattt	aaggaaagat	17897
acggtgtttc	gcctgtctcc	ttggtgaggc	aggcttgatt	tcccatagcg	ttattgcgggt	17957
cgtcgttgca	aatgcggacc	tgcgtgatca	tcaaggctaa	gactgccaca	ttaggtgtcg	18017
actcgagcgt	ccctctatcc	gcctgacgc	gctccgtccc	tagtacctag	gaaattgagt	18077
gggcctactt	gccagggcca	gttggaattcg	gtgctggtga	gcgctgcggg	tgacagaatc	18137

ctgatcgtgg	cgatcacgat	ggcgataaag	ttgcccggtg	tcgtagatcg	cagggtgacc	18197
aagacgggga	ctcatggcgc	ggatccccgc	agtgatgcct	tcgcatgacg	ccacctctct	18257
cctccgctca	gccttcatgc	ctgactaatt	aagtcgtata	tcaatctggc	tctgtgccgc	18317
attcagttcc	tccagctgca	ttgtctctcg	gcgggagggc	attccccctgc	attggccaaa	18377
tgggtccct	tgttcacgac	cggacaagcg	caccgtgctg	cccgttcgtc	gtgtgccctg	18437
tcaaaaagcc	tggcgacgaa	agggcggcag	gccgcatggc	cacggctggg	cggtaactga	18497
tgcttgcggt	aatcgttaac	cgtttgaaat	tccttgccaa	atttcggcga	gagaatcatg	18557
cgggtacgcc	tttcogtgcg	ctttgatctg	cgcttcogtg	cottgaatca	gaaaaatagt	18617
taattgacag	aactataggt	tcgcagtagc	ttttgtcac	ccaccaaate	cacagcactg	18677
gggtgcacga	tgaatagcta	cgatggccgt	tggctctaccg	ttgatgtgaa	ggttgaagaa	18737
ggtatcgctt	gggtcacgct	gaaccgcccg	gagaagcgca	acgcaatgag	cccaactctc	18797
aatcgagaga	tggtcgaggt	tctggaggtg	ctggagcagg	acgcagatgc	tcgctgctt	18857
gttctgactg	gtgcaggcga	atcctggacc	gcgggcatgg	acctgaagga	gtatttccgc	18917
gagaccgatg	ctggccccga	aattctgcaa	gagaagattc	gtcgcgaagc	gtcgacctgg	18977
cagtggaagc	tcctgcggat	gtacaccaag	ccgaccatcg	cgatgggtcaa	tggctgggtgc	19037
ttcggcggcg	gcttcagccc	gctgggtggc	tgtgatctgg	ccatctgtgc	cgacgaggcc	19097
acctttggcc	tgtccgagat	caactggggc	atcccgcggg	gcaacctggt	gagtaaggct	19157
atggccgaca	ccgtgggtca	ccgcgagtcc	ctttactaca	tcatgactgg	caagacattt	19217
ggcggtcagc	aggccgccaa	gatggggctt	gtgaaccaga	gtgttcogct	ggccgagctg	19277
cgcagtgtca	ctgtagagct	ggctcagaac	ctgctggaca	agaaccccg	agtgtctgct	19337
gccgccaaaa	taggcttcaa	gcgttgccgc	gagctgactt	gggagcagaa	cgaggactac	19397
ctgtacgcca	agctcgacca	atcccgtttg	ctcgatccgg	aaggcggctg	cgagcagggc	19457
atgaagcagt	tccttgacga	gaaaagcatc	aagccgggct	tgcagacct	caagcgctga	19517
taaatgcgcc	ggggccctcg	ctgcgcccc	ggccttccaa	taatgacaat	aatgaggagt	19577
gccaatgtt	tcacgtgccc	ctgcttattg	gtggtgaagc	ttgttcagca	tctgatgagc	19637
gcaccttcga	gcgtcgtage	ccgctgaccg	gagaagtgg	atcgcgcgct	gctgctgcc	19697
gtttggaaga	tgcggacgcc	gcagtggccg	ctgcacaggc	tgcgtttcct	gaatgggagg	19757
cgcttgctcc	gagcgaacgc	cgtgcccgc	tgctgcgagc	ggcggatcct	ctagaggacc	19817
gttcttccga	gttcaccgcc	gcagcgagtg	aaactggcgc	agcgggaaac	tggtatgggt	19877

ttaacgttta cctggcggcg ggcattgtgc gggaagccgc ggccatgacc acacagattc 19937  
 agggcgatgt cattccgtcc aatgtgcccg gtagctttgc catggcggtt cgacagccat 19997  
 gtggcggtgt gctcggattt gcgccttgga atgctccggt aatccttggc gtacgggctg 20057  
 ttgcgatgcc gttggcatgc ggcaataccg tgggtgtgaa aagctctgag ctgagtcctt 20117  
 ttacccatcg cctgatttgt caggtgttgc atgatgctgg tctgggggat ggcgtggtga 20177  
 atgtcatcag caatgccccg caagacgctc ctgcggttgt ggagcgactg attgcaaata 20237  
 ctgcggtacg tcgagtgaac ttcaccggtt cgaccacagt tggacggatc attggtgagc 20297  
 tgtctgcgcg tcatctgaag cctgctgtgc tggaaattagg tggtaaggct ccgttcttgg 20357  
 tcttggaaga tgccgacctc gatgcggcgg tcgaagcggc ggccttttgt gcctacttca 20417  
 atcagggtca aatctgcatg tccactgagc gtctgattgt gacagcagtc gcagacgcct 20477  
 ttgttgaaaa gctggcgagg aaggtcgcca cactgcgtgc tggcgatcct aatgatccgc 20537  
 aatcgggtctt gggttcgttg attgatgcca atgcagggtc acgcatccag gttctggtcg 20597  
 atgatgcgct cgcaaaaggc gcgcggcagg tcgtcgggtg tggcttagat ggcagcatca 20657  
 tgcagccgat gctgcttgat caggtcactg aagagatgag gctctaccgt gaggagtcct 20717  
 ttggccctgt tgccgttgct ttgcgcggcg atggtgatga agaactgctg cgtcttgcca 20777  
 acgattcgga gtttggtctt tcggccgcca ttttcagccg tgacgtctcg cgcgcaatgg 20837  
 aattggccca gcgcgtcgat tcgggcattt gccatatcaa tggaccgact gtgcatgacg 20897  
 aggctcagat gccattcggg ggggtgaagt ccagcggcta cggcagcttc ggcagtcgag 20957  
 catcgattga gcactttacc cagctgcgct ggctgaccat tcagaatggc ccgcggcact 21017  
 atccaatcta aatcgatctt cgggcgcccgc gggcatcatg cccgcggcgc tcgcctcatt 21077  
 tcaatctcta acttgataaa aacagagctg ttctccggtc ttggtggatc aaggccagtc 21137  
 gcggagagtc tcgaagagga gactacagtg aacgccgagt ccacattgca accgcaggca 21197  
 tcatcatgct ctgctcagcc acgctaccgc agtgtgtcga ttggtcatcc tccggttgag 21257  
 gttacgcaag acgctggagg tattgtccgg atgcgttctc tcgaggcgct tcttcccttc 21317  
 ccgggtcgaa ttcttgagcg tctcgagcat tgggctaaga cccgtccaga acaaacctgc 21377  
 gttgctgcca gggcgcaaaa tggggaatgg cgtcgtatca gctacgcgga aatgttccac 21437  
 aacgtccgcg ccatcgaca gagcttgctt ccttacggac tatcggcaga gcgtccgctg 21497  
 cttatcgtct ctggaaatga cctggaacat cttcagctgg catttggggc tatgtatgag 21557

ggcattccct attgcccggt gtctcctgct tattcaactgc tgtcgcaaga tttggcgaag 21617  
 ctgcgtcaca tcgtaggtct tctgcaaccg ggactgggtct ttgctgccga tgcagcacct 21677  
 ttccagcgcg caattgagac cattctgccg gacgacgtgc ccgcaatctt cactcgaggc 21737  
 gaattggccg ggcgggcgac ggtgagtttt gacagcctgc tggagcagcc tgggtgggatt 21797  
 gaggcagata atgcctttgc ggcaactggc cccgatacga ttgccaaagt cttgttcact 21857  
 tctggctcta ccaaactgcc taaggcggtg ccgactactc agcgaatgct ctgcgccaat 21917  
 cagcagatgc ttctgcaaac tttcccggtt tttggtgaag agccgccggt gctggtggac 21977  
 tggttgccgt ggaaccacac cttcggcggc agccacaaca tcggcatcgt gttgtacaac 22037  
 ggcggcacgt actaccttga cgacggtaaa ccaaccgccc aagggttcgc cgagacgctt 22097  
 cgcaacttga gcgaaatctc tcccactgcg tacctcactg tgccgaaagg ctgggaggaa 22157  
 ttagtggttg cccttgagcg agacagtacc ctgcgcgaaac gcttcttcgc tcgcatgaag 22217  
 ctgttcttct tcgcggcggc tgggttgctg caagggatct gggatcgttt ggaccgggtc 22277  
 gctgaacagc actgtggtga gcgcattcgc atgatggcgg gtctgggcat gacggagact 22337  
 gtccttcct gcacttttac caccggaccg ctgtcgatgg ctggttacat tgggctgcca 22397  
 gcgcctggct gcgaggtaa gctcgttccg gtcgatggga aattggaagg gcgtttccat 22457  
 ggtccgcacg tcatgagcgg ctactggcgt gtcctgaac aaaatgcca agcgttcgac 22517  
 gaggaaggct attactgctc cggatgatgc atcaaattgg cagatcctgc cgatcctcag 22577  
 aaaggctctga tgtttgacgg tcgaattgct gaagacttca agctgtcctc aggggtatct 22637  
 gtcagcggtg ggccattgcg caccggggcg gttctggaag gcggctctta cgtcctggac 22697  
 gtagtggttg ctgctcctga tcgtgaatgc cttggattgc tcgtgtttcc gcgtcttctc 22757  
 gactgccgtg ccttgctcgg gctaggaaaa gaggcgtcgg acgccgaggt gcttgccagt 22817  
 gagccggttc gggcctggtt tgctgactgg ctcaaacgac tcaatcgaga agcaactggc 22877  
 aatgccagtc gcatcatgtg ggtagggctc ctcgatacgc cgccgtcgat tgataagggc 22937  
 gaggtcactg acaagggtc gatcaaccag cgcgctgttt tgcaatggcg gtcggcgaaa 22997  
 gttgatgcgc tgtatcgtgg tgaagatcaa tccatgctgc gtgacgaggc cacactgtga 23057  
 gttggtcagg gggggccttac tcggcgtttt ccgacactgc gttggttgcg gcagtgcgca 23117  
 cccctggat tgattgcggg ggtgccctgt cgctggtgtc gcctatcgac ttaggggtaa 23177  
 aggtcgctcg cgaagttctg atgcgtgcgt cgcttgaacc acaaattggtc gatagcgtag 23237  
 tcgcaggctc tatggctcaa gcaagctttg atgcttacct gctcccgcg cacattggct 23297

tgtagacgcgg	tggtcccaag	tcggtttcgg	ccttgggggt	gcagcgcatt	tgcggcacag	23357
gcttcgaact	gcttcggcag	gccggcgagc	agatttccca	aggcgtgat	cacgtgctgt	23417
gtgtcgcggc	agagtccatg	tcgcgtaacc	ccatcgcgtc	gtatacacac	cggggcgggt	23477
tccgcctcgg	tgcgcccgtt	gagttcaagg	atTTTTtgtg	ggaggcattg	tttgatcctg	23537
ctccaggact	cgacatgata	gctaccgcag	aaaacctggc	gcgcctgtac	ggaatcacca	23597
ggggagaagc	taattccctac	gcggtaagca	gcttcgagcg	cgcattgagg	gcgcaagagg	23657
agaaatggat	tgaccaagag	atcgtggctg	ttacggatga	acagttcgat	ttagagggct	23717
acaacagtcg	agcaattgaa	ctgcctcggg	aggcaaaatt	gttgatcgtg	acagtcatcc	23777
gcggcctagc	agtctttgaa	gccctttccc	gattgaagcc	tgttcattct	ggcgggggtg	23837
agactgcggg	caacagctgt	gccgtagtgg	acggcgccgc	ggcggctttg	gtggctcgag	23897
agtcgtctgc	gacacagccg	gtcttggcta	ggatactggc	tacctccgta	gtcgggatcg	23957
agcccgagca	tatggggctc	ggccctgcgc	ccgcgattcg	cctgctgctt	gcgcgtagtg	24017
atcttagttt	gagggatata	gacctctttg	agataaacga	ggcgcaggcc	goccaaagttc	24077
tagcgggtaca	gcatgaattg	ggtattgagc	actcaaaact	taatatttgg	ggcggggcca	24137
ttgcacttgg	acacccgctt	gccgcgaccg	gattgcgtct	ctgcatgacc	ctcgctcacc	24197
aattgcaagc	taataacttt	cgatatggaa	ttgcctcggc	atgcattggg	gggggacagg	24257
ggatggcggg	tcttttagag	aatccccact	tcggttcgtc	ctctgcacga	agttcgatga	24317
ttaacagagt	tgaccactat	ccactgagct	aacgggcata	tcctttgttg	ctttgaggtg	24377
gcgcacgaag	gagggctcga	aaatctctgc	taaaaacaag	aagaaggaac	aggggaacatg	24437
attagtttgc	ctcgatatgg	agaaagttta	ggagtccagg	ctaaaacttg	ccttgcccttc	24497
gcactcgtat	tatgtgtcgg	gctgattgtt	accggcacgg	gtttctacag	tgtacatacc	24557
ttgtcagggg	tggtggaaaa	gagcgcgata	gctggtgagt	tgcgggcgaa	aattcaggaa	24617
ctgaagggttc	tggagcagcg	cgccttattc	atcgccgatg	aagggtcgct	gaagcagcgc	24677
tcgatcctcc	taagtcaggg	gatagctgaa	gttaatgatg	ctatagatat	ttttgacttt	24737
cagcgcggac	gatctgagtt	acttaaattc	gctgcttctt	cgcgcgaagc	aagttactcc	24797
attgaggtcg	gtagtaacgc	tcgggccgat	aagttgcagt	cgggcgaacc	aagtgacgca	24857
ttgatgggtg	ccgataaaaa	gctgaatgtt	gagtatgagc	aattgagttc	tgctgtgaat	24917
gcactgatgg	ggcatttaat	tgaggatcag	aatgaaaaag	ttccactaat	ctactatatg	24977



cttggcgggcg	taacttttgtt	tacgatgctc	atgagtgcctt	attcgggtctg	gttcattttcg	25037
cgtcagtttag	ttccgccatt	aaagtgcgacg	gtgcagccttg	ccgagcggat	tgcatacaggc	25097
gacttggtctg	atgtcgggga	cagcaggcgc	aaggatgaaa	tcgggtcagtt	gcaaagtgc	25157
actaggcgga	tggcgatttg	actgcgtaat	ctggtcggtg	atattgggtca	aagtcgtgcg	25217
caactggttt	catcgtccag	cgacctttcg	gccatctgtg	ctcagggtca	gattgatgtc	25277
gagtgccaga	agctttcggg	cgcccaggtc	tctaccgccg	tgaacgagtt	ggttgaaacc	25337
gtccaggcaa	tagcaaaaag	caccgaagag	gcagcaacag	tcgccgtctt	ggccgatgaa	25397
aaggcacgcg	gtggtgaaag	tgtcgttaac	aaggccgttg	atttcattga	gcacctctcc	25457
ggagatatgg	cggaactggg	agacgcaatg	gagcggcttc	agaacgacag	tgcgcagatc	25517
aataaggtag	tagacgtcat	taaggctgtg	gcggagcaga	ccaatctgct	agccctgaat	25577
gcggcgatag	aggcggcccc	tgcaggagag	cagggcaggg	gcttttgcgg	cgtggcggat	25637
gaggttcgtg	ctttggcgat	gcgcacccaa	caatcgacca	aagaaattga	gaggctagt	25697
gtttcattgc	agcagggaag	tgaagctgcg	ggcgagttga	tgcggcggtg	caagggtccg	25757
acgcatgacg	tcgttggatt	ggcccagcaa	gccgcgcgcc	gcgctactcg	aaattaccca	25817
gctgtcgccg	gcatccaagc	gatgaactat	cagatcgccg	ctggagcaga	gcagcaaggg	25877
gctgctgtgg	ttcaaataca	ccagaatatg	cttgaagtgc	ataagatggc	tgacgagtcc	25937
gccattaaag	cgggacagac	catgaagtca	tcgaaggagc	ttgctcacct	cggcagtgcg	25997
ctacaaaaat	ccgttgatcg	attccagctg	tagcgcctcg	ggtggctgaa	acgcgcattt	26057
tcgttaaggt	cttcagcgcg	gtctgctggg	gcgtggggccg	ctagcctaac	tgttgcgctt	26117
caggctccgc	atggatcttg	tgcagcagca	atagcaattg	ttcacgttcg	tcatcactca	26177
gcatcgacgt	cgcgtcttgg	tcgctctgta	ccacgatctt	cttcagctct	ttgagctgcg	26237
tctccccagc	tttgctgaga	aatatcccat	aggaacgctt	gtccggccttg	cagcgcacgc	26297
gcacagcaag	gccgagcttc	tcgagcttgt	tcagcaaggg	aaccagttgt	ggtggttcga	26357
ttgcgagcat	ccgcgctagg	tcagcctgca	taagcccagg	gctcgcttcg	atgattagaa	26417
gtgccgacag	ctgcgcgggg	cgtaggtcat	atggcgtcag	ggcttcaatc	aggccctgag	26477
cgagcttcag	ctgtgagccg	gcgtaaggca	tagccaatca	attgattcag	gagcgtatcg	26537
cccggttcta	tcagcggggc	gcttttcgaaa	gtcatggtgt	tagccggtag	ggtctttttc	26597
ttggccatgc	ttgttgccctg	aaccttcggt	gacatagggc	agaggtgcgt	ttgccgcttc	26657
gcttcgcgat	gaaccgcata	gagatgctga	ggtcaggatt	tttccttaac	tcgcgtaagc	26717

attctgtcat	ttttttggtg	gctttgaaca	gcctgatgaa	aggtggtctc	gccctttgag	26777
gccgattctt	gggcgcttgg	cggcgctgaa	gcgatgctcc	actaccgatt	aagataatta	26837
aaataaggaa	accgcatggt	ttcttatgtg	aatttgtctg	gcatactcca	gctcaagggc	26897
aatttttggg	ctattggctg	agcagttgcc	tctatatggt	tattcagaat	aacaattgac	26957
tcctcaggag	gtcagcgatg	agcattcttg	gtttgaatgg	tgccccgggc	ggagctgagc	27017
agctggggctc	ggctcttgat	cgcataga	aggcgcacct	ggagcagggg	cctgcaaact	27077
tggagctgcg	tctgagtagg	ctggatcgtg	cgattgcaat	gcttctggaa	aatcgtgaag	27137
caattgccga	cgcggtttct	gctgactttg	gcaatcgag	ccgtgagcaa	acactgcttt	27197
gcgacattgc	tggctcgggtg	gcaagcctga	aggatagccg	cgagcacgtg	gccaaatgga	27257
tggagcccga	acatcacaag	gcgatgtttc	caggggcgga	ggcacgcggt	gagtttcagc	27317
cgctgggtgt	cgttgggggc	attagtcctt	ggaacttccc	tatcgtagctg	gcctttgggc	27377
cgctggccgg	catattcgca	gcaggtaatc	gcgccatgct	caagccgtcc	gagcttacct	27437
cgcggacttc	tgccctgctt	gcggagctaa	ttgctcgtaa	cttcgatgaa	actgagctga	27497
ctacagtgtc	gggcgacgct	gaagtcgggtg	cgctgttcag	tgctcagcct	ttcgatcatc	27557
tgatcttcac	cggcggcact	gccgtggcca	agcacatcat	gcgtgccgcg	gcggataacc	27617
tagtgcccgt	taccctggaa	ttgggtggca	aatcgccggt	gatcgtttcc	cgcagtgcag	27677
atatggcgga	cgttgcacaa	cgggtgttga	cggtgaaaac	cttcaatgcc	gggcaaactc	27737
gtctggcacc	ggactatgtg	ctgctgccgg	aagaatcgct	ggatagcttt	gtcgccgagg	27797
cgacgcgctt	cgtggccgca	atgtatccct	cgcttctaga	taatccggat	tacacgtcga	27857
tcatcaatgc	ccgaaatttc	gaccgtctgc	atcgctacct	gactgatgcg	caggcaaagg	27917
gagggcgcg	cattgaaatc	aatcctgcgg	ccgaagagtt	gggggatagt	ggtatcagga	27977
agatcgcgcc	cactttgatc	gtgaatgtgt	cggatgaaat	gctggctctg	aacgaggaga	28037
tctttggtcc	gctgctcccg	atcaagactt	atcgtagattt	cgactcggct	atcgactacg	28097
tcaacagcaa	gcagcgacca	cttgccctcg	acttcttcgg	cgaagatgcg	gttgagcggtg	28157
agcaagtgtc	taagcgtagc	gtttcggggc	ccgtgggtcg	gaacgatgtc	atgagccatg	28217
tgatgatgga	tacgcttcca	tttggtggtg	tggggcactc	gggggatggg	gcataatcacg	28277
gcatttatgg	tttccgaacc	ttcagccatg	ccaagcctgt	tctcgtgcaa	agtcctgtgg	28337
gtgagtcgaa	cttggcgatg	cgcgcaccct	acggagaagc	gatccacgga	ctgctctctg	28397

tcctcctttc aacggagtgt tagaaccgtt ggtagtggtt ttggacgggc ccaggagcat 28457  
gcgcttcttg gcccgtttct tgagtattca ttggatagtc acgcgtggta gcttcgagcc 28517  
tgcacagctg atgagcacc tgggaaggcg gctgtacgag gacgactggg ttcattcttcg 28577  
ccattcatga cggaactccg ttccccagta ccgcgatgac tattttgcct cttccgatgt 28637  
ccgattccac gccgcctgac gctaagcggg ggcgggggcg cccgcacccc agcccagaca 28697  
gcaacaaatg agtaggctct tggatgccgc ggcggtgag attggtaacg gcaatttcgt 28757  
caatgtgacg atggattcga ttgcccggtc tgccggcgtc tcaaaaaaaaa cgctgtacgt 28817  
cttggtggcg agcaaggaag aactcatttc ccggttagtg gctcgagaca tgtccaacct 28877  
tgagctgctg ctttgtcacg aggttgagtc tgcggaggcc cttcaggatg agttgcgaaa 28937  
ctatctgctg ctctggggcg gcttgacctt gtccccctct gctttgggca tttttctgat 28997  
ggccgtgcag gggcgtagaa gtgccccggg cctggcgaga atctggtatc gagagggggc 29057  
agagcgttgc ctcagcttgc ttcggggatg gttggcaagg atggcaagcc gggagctgat 29117  
cgctcctgga gatatcgact ccgcagtgga gcttatcgat tcgctcctga tctcacagcc 29177  
tttgaaatta tttggcctgg ggatccagag cggtcgacc gatgatcaga tcaatcaacg 29237  
ggtcacaatc gctctcgatg cattccgtcg gtgctatgtc gtttagcacc gttctcgagg 29297  
gctgtggcgg cgtgacctat ttgtctagtg gtccggcgga aattcgataa gaaagctggg 29357  
cgcgagtgag gccgagccgg cgggcagctt ccgagacatt gcctttcacc tggcccagag 29417  
catggctaata catcgcgctc tccacttctt gcagcgctcat cgcgctcagg tcctttgagt 29477  
caagcggcga gtcgattgtg ctggtcgggt tggagaagga agtacttggg ctgccagttt 29537  
cctgtggctg attatcttga gcggtggcca ggatgccgt ggccccaatg gagaacatcg 29597  
gttgagtcag tcgttcaccg ctagtgaaga ggtggctcac gtcaatggct ccatcctccg 29657  
gagcgctgat gactccgagc tccaccaaata tttgaagctc ccggatgttt cctggaaagt 29717  
cgtagccaag cagggcattg gctgcacgtg gagtgaatcc gctgaccacc cggctatgac 29777  
gctgattgaa gcggtgcagg aaataggtca tcaggagggg aatgtcttcc ttcctctctc 29837  
gaagcggcgg gaggtggatc gggtaaacat tgaggcgga aaaaaggctc tcgcggaact 29897  
cgccgcgctg gacgcctgag cgaagatcga cattgggtgc ggctaccaca cggacgtcaa 29957  
ccttgagtgt cctgcttccg ccaaccctgt cgacctccga ctcttgaggg gcgcgaagta 30017  
acttcccttg ggccacgagg cttagcgctc ctatctcgtc aaggaatagt gtgccgccc 30077  
aagcgcgctc gaaccgtcct gctcgagatt ggggtggcgcc ggtaaagccc ccccgttcga 30137

cgccgaacaa ctcggactcc atcaggggtt cggaataacg tgcgcaattg accgcaacaa 30197  
acggggccgtc gtgtctgggg ctgatgcggg gaagcatgcg ggcgaacatc tccttgccca 30257  
cacctgattc acccgtaaac agtaccgtcg cctccgtggg tgctacgcgc ttcagcatgt 30317  
ggcaggcagc attgaatgcc gaggaaatc ccaccatgtc gtgttccgat gcagtgcctg 30377  
agtctgcggc ggagtgatgg ggagtgttcc tttgtccctg ctgcgttctt cgtctctgcg 30437  
gcggtgcttg ttgccgacaa atgggtgcgc taagcgccgc caagtcctct tcggcgctctt 30497  
cccattcttc cgctggcttg ccgatcatgc ggcagatctg cgaaccctg gagcggcatt 30557  
ccacctctcg gtaaaggatg aggcgaccaa ccagcgcgga cgtatagcca atggcataac 30617  
ccgtctgcgt ccagcacgcg ggctcggtgc cgatgccgta gtgcgcaata tgttcatcat 30677  
cttcgctcga atggtgccag aggaattcgc cgtagtaggt ccccaaattc atgtcgaagt 30737  
cgaagtggat cggctccacg cgtactgcgc cttccagaga gtgcaagtcc gggccggcgg 30797  
caaataggga gagcggatcg gcgttgctga agcgcctcct cagaaggcg gcattcttg 30857  
cgccgcagtg gtaaccggtt cgcagcatga ttccgcgggc gcgggcgaag cccacgcttt 30917  
caattaattc gcgtcgcaat gcacccagtc cgctgctgtg gaggagcagc attcgcgcgc 30977  
cgttcaacca gatgcgtcca tcgccagggc tgaaaaggag ggattcagtg aggtcatgaa 31037  
gggagggggac gggcgcctggc tccaattgct cgatggcgcc gcgattgagt gtcttgggcg 31097  
cggctcttga gagttcggct agggagataa atttgctggc catggtggcg gccctgatg 31157  
ggttgatga ttttctgcat tctgcatcat gaaattcatg aaatcatcac ttttcggggg 31217  
gtgggtgcac gggattgaag gttgctagga gagtgcattg ctcgtaagcc caggaagcac 31277  
gcgggtttca ggatggtgca tggaaatggc atgagctttg ctggatatga ttagagacat 31337  
taactatattt ggcggaatgg aagcacgatt cctcgcccgg tagagcggta accgcgacat 31397  
tcaggaccgt aaaaaggaaa gagcatgcaa ctgaccaaca agaaaatcgt cgtcaccgga 31457  
gtgtcctccg gtatcggtgc cgaaactgcc cgcgttctgc gctctcacgg cgccacagtg 31517  
attggcgtag atcgcaacat gccgagcctg actctggatg ctttcgttca ggctgacctg 31577  
agccatcctg aaggcatcga taaggccatc tctcagctgc cggagaaaat tgacggactc 31637  
tgcaatatcg ccggggtgcc cggcactgcc gatcctcagc tcgtcgcaaa cgtgaactac 31697  
ctgggtctaa agtatctgac cgaggcagtc ctgtcgcgca ttcaaccogg tggttcgatt 31757  
gtcaacgtgt cctctgtgct tggcgccgag tggccggccc gccttcagtt gcataaggag 31817

ctggggagtg ttgttggatt ctccgaaggc caggcatggc ttaagcagaa tccagtggcc 31877  
 cccgaattct gctaccagta tttcaaagaa gcaactgatcg tttggtctca agttcaggcg 31937  
 caggaatggg tcatgaggac gtctgtacgc atgaactgca tcgcccccg ccctgtattc 31997  
 actcccattc tcaatgagtt cgtcaccatg ctgggtcaag agcggactca ggcggacgct 32057  
 catcgtatta agcggccagc atatgccgat gaagtggccg cgggtgattgc attcatgtgt 32117  
 gctgaggagt cacgttggat caacggcata aatattccag tggacggagg tttggcatcg 32177  
 acctacgtgt aagttcgtgg acgccctttg cagcgcact atatctctat gcagcagctg 32237  
 aaagcagctt tggttttgat cggaggtagc gggcggaaaag gtgcagaatg tctaaataat 32297  
 aaaggattct tgtgaagctt tagttgtccg taaacgaaaa taaaaataaa gaggaatgat 32357  
 atgaaagcaa gtagatcagt ctgcactttc aaaatagcta ccctggcagg cgccatttat 32417  
 gcagcgctgc caatgtcagc tgcaaaactcg atgcagctgg atgtaggtag ctcggattgg 32477  
 acggtgcgtt ggggacaaca ccctcaagta tagccttgcc tctcgctga atgagcaaga 32537  
 ctcaagtctg acaaatgcgc cgactgtcaa tggttatatc cggatattca aagtcagggt 32597  
 gatcgtaact ttgaccgggg gcttgggtatc caatcgtctc gatattctgt cggagcttga 32657  
 tgtcagtcgt gactggttgg tg 32679

<210> 2

<211> 284

<212> PRT

<213> Pseudomonas sp.

<400> 2

Met	Ile	Ala	Ile	Thr	Gly	Ala	Ser	Gly	Gln	Leu	Gly	Arg	Leu	Thr	Ile
1				5					10					15	
Glu	Ala	Leu	Leu	Lys	Arg	Leu	Pro	Ala	Ser	Glu	Ile	Ile	Ala	Leu	Val
			20					25					30		
Arg	Asp	Pro	Asn	Lys	Ala	Gly	Asp	Leu	Thr	Ala	Arg	Gly	Ile	Val	Val
		35					40					45			
Arg	Gln	Ala	Asp	Tyr	Asn	Arg	Pro	Glu	Thr	Leu	His	Arg	Ala	Leu	Ile
	50					55					60				
Gly	Val	Asn	Arg	Leu	Leu	Leu	Ile	Ser	Ser	Ser	Glu	Val	Gly	Gln	Arg
65				70						75					80
Thr	Ala	Gln	His	Arg	Ala	Val	Ile	Asp	Ala	Ala	Lys	Gln	Glu	Gly	Ile
			85						90					95	
Glu	Leu	Leu	Ala	Tyr	Thr	Ser	Leu	Leu	His	Ala	Asp	Lys	Ser	Ala	Leu
			100					105					110		



tat	cgg	ggg	ccg	gaa	gga	cgt	gtt	gcc	gcg	gta	gag	gat	ttc	tgc	cct	144
Tyr	Arg	Gly	Pro	Glu	Gly	Arg	Val	Ala	Ala	Val	Glu	Asp	Phe	Cys	Pro	
		35				40						45				
cat	cgc	ggg	gca	ccg	ttg	tcc	ctg	ggt	ttc	gtt	cgc	gac	ggg	aag	ctg	192
His	Arg	Gly	Ala	Pro	Leu	Ser	Leu	Gly	Phe	Val	Arg	Asp	Gly	Lys	Leu	
		50				55						60				
att	tgc	ggc	tac	cac	ggt	ttg	gaa	atg	ggc	tgc	gag	ggc	aaa	acg	ctc	240
Ile	Cys	Gly	Tyr	His	Gly	Leu	Glu	Met	Gly	Cys	Glu	Gly	Lys	Thr	Leu	
		65				70						75		80		
gcg	atg	ccc	ggg	cag	cgc	gtt	caa	ggc	ttc	cct	tgc	atc	aaa	agc	tac	288
Ala	Met	Pro	Gly	Gln	Arg	Val	Gln	Gly	Phe	Pro	Cys	Ile	Lys	Ser	Tyr	
				85						90				95		
gcg	gta	gaa	gag	cga	tac	ggc	ttt	atc	tgg	gta	tgg	cct	ggg	gat	cgc	336
Ala	Val	Glu	Glu	Arg	Tyr	Gly	Phe	Ile	Trp	Val	Trp	Pro	Gly	Asp	Arg	
		100						105						110		
gag	ctg	gcg	gat	ccg	gcg	ctt	att	cac	cac	ctg	gag	tgg	gcc	gat	aat	384
Glu	Leu	Ala	Asp	Pro	Ala	Leu	Ile	His	His	Leu	Glu	Trp	Ala	Asp	Asn	
		115				120						125				
ccg	gag	tgg	gcc	tat	ggt	ggc	ggt	ctc	tac	cac	atc	gct	tgt	gat	tac	432
Pro	Glu	Trp	Ala	Tyr	Gly	Gly	Gly	Leu	Tyr	His	Ile	Ala	Cys	Asp	Tyr	
		130				135						140				
cgc	ctg	atg	atc	gac	aac	ctc	atg	gat	ctc	acc	cat	gag	acc	tat	gtg	480
Arg	Leu	Met	Ile	Asp	Asn	Leu	Met	Asp	Leu	Thr	His	Glu	Thr	Tyr	Val	
		145				150				155				160		
cat	gcc	tcc	agc	atc	ggt	caa	aag	gaa	att	gac	gag	gca	ccg	gtc	agt	528
His	Ala	Ser	Ser	Ile	Gly	Gln	Lys	Glu	Ile	Asp	Glu	Ala	Pro	Val	Ser	
				165						170				175		
act	cgt	gtc	gag	ggc	gac	acc	gtg	att	acc	agc	cgg	tac	atg	gat	aac	576
Thr	Arg	Val	Glu	Gly	Asp	Thr	Val	Ile	Thr	Ser	Arg	Tyr	Met	Asp	Asn	
		180						185						190		
gtc	atg	gcc	cct	ccg	ttc	tgg	cgt	gct	gcg	ctt	cgt	ggc	aac	ggc	ttg	624
Val	Met	Ala	Pro	Pro	Phe	Trp	Arg	Ala	Ala	Leu	Arg	Gly	Asn	Gly	Leu	
		195				200						205				
gcc	gac	gat	gta	ccg	gtt	gat	cgc	tgg	cag	atc	tgc	cga	ttc	gct	cct	672
Ala	Asp	Asp	Val	Pro	Val	Asp	Arg	Trp	Gln	Ile	Cys	Arg	Phe	Ala	Pro	
		210				215						220				
ccg	agt	cac	gta	ctg	atc	gaa	gta	ggt	gtg	gct	cat	gcg	ggc	aaa	ggc	720
Pro	Ser	His	Val	Leu	Ile	Glu	Val	Gly	Val	Ala	His	Ala	Gly	Lys	Gly	
		225				230				235				240		
gga	tat	gac	gcg	ccg	gcg	gaa	tac	aag	gcc	ggc	agc	ata	gtg	gtc	gac	768
Gly	Tyr	Asp	Ala	Pro	Ala	Glu	Tyr	Lys	Ala	Gly	Ser	Ile	Val	Val	Asp	
		</														

ttc atc acg ccg gag agt gat acc tcg att tgg tac ttc tgg ggc atg	816
Phe Ile Thr Pro Glu Ser Asp Thr Ser Ile Trp Tyr Phe Trp Gly Met	
260 265 270	
gct cgc aac ttc cgt ccg cag ggc acg gag ctg act gaa acc att cgt	864
Ala Arg Asn Phe Arg Pro Gln Gly Thr Glu Leu Thr Glu Thr Ile Arg	
275 280 285	
gtt ggt cag ggc aag att ttt gcc gag gac ctg gac atg ctg gag cag	912
Val Gly Gln Gly Lys Ile Phe Ala Glu Asp Leu Asp Met Leu Glu Gln	
290 295 300	
cag cag cgc aat ctg ctg gcc tac ccg gag cgc cag ttg ctc aag ctg	960
Gln Gln Arg Asn Leu Leu Ala Tyr Pro Glu Arg Gln Leu Leu Lys Leu	
305 310 315 320	
aat atc gat gcc ggc ggg gtt cag tca cgg cgc gtc att gat cgg att	1008
Asn Ile Asp Ala Gly Gly Val Gln Ser Arg Arg Val Ile Asp Arg Ile	
325 330 335	
ctc gca gct gaa caa gag gcc gca gac gca gcg ctg atc gcg aga agt	1056
Leu Ala Ala Glu Gln Glu Ala Ala Asp Ala Ala Leu Ile Ala Arg Ser	
340 345 350	
gca tca tga	1065
Ala Ser	
<210> 4	
<211> 354	
<212> PRT	
<213> not required under old rule	
<400> 4	
Met Phe Pro Lys Asn Ala Trp Tyr Val Ala Cys Thr Pro Asp Glu Ile	
1 5 10 15	
Ala Asp Lys Pro Leu Gly Arg Gln Ile Cys Asn Glu Lys Ile Val Phe	
20 25 30	
Tyr Arg Gly Pro Glu Gly Arg Val Ala Ala Val Glu Asp Phe Cys Pro	
35 40 45	
His Arg Gly Ala Pro Leu Ser Leu Gly Phe Val Arg Asp Gly Lys Leu	
50 55 60	
Ile Cys Gly Tyr His Gly Leu Glu Met Gly Cys Glu Gly Lys Thr Leu	
65 70 75 80	
Ala Met Pro Gly Gln Arg Val Gln Gly Phe Pro Cys Ile Lys Ser Tyr	
85 90 95	
Ala Val Glu Glu Arg Tyr Gly Phe Ile Trp Val Trp Pro Gly Asp Arg	
100 105 110	
Glu Leu Ala Asp Pro Ala Leu Ile His His Leu Glu Trp Ala Asp Asn	
115 120 125	



```

Pro Glu Trp Ala Tyr Gly Gly Gly Leu Tyr His Ile Ala Cys Asp Tyr
 130                      135                      140

Arg Leu Met Ile Asp Asn Leu Met Asp Leu Thr His Glu Thr Tyr Val
 145                      150                      155                      160

His Ala Ser Ser Ile Gly Gln Lys Glu Ile Asp Glu Ala Pro Val Ser
                      165                      170                      175

Thr Arg Val Glu Gly Asp Thr Val Ile Thr Ser Arg Tyr Met Asp Asn
                      180                      185                      190

Val Met Ala Pro Pro Phe Trp Arg Ala Ala Leu Arg Gly Asn Gly Leu
                      195                      200                      205

Ala Asp Asp Val Pro Val Asp Arg Trp Gln Ile Cys Arg Phe Ala Pro
 210                      215                      220

Pro Ser His Val Leu Ile Glu Val Gly Val Ala His Ala Gly Lys Gly
 225                      230                      235                      240

Gly Tyr Asp Ala Pro Ala Glu Tyr Lys Ala Gly Ser Ile Val Val Asp
                      245                      250                      255

Phe Ile Thr Pro Glu Ser Asp Thr Ser Ile Trp Tyr Phe Trp Gly Met
                      260                      265                      270

Ala Arg Asn Phe Arg Pro Gln Gly Thr Glu Leu Thr Glu Thr Ile Arg
                      275                      280                      285

Val Gly Gln Gly Lys Ile Phe Ala Glu Asp Leu Asp Met Leu Glu Gln
 290                      295                      300

Gln Gln Arg Asn Leu Leu Ala Tyr Pro Glu Arg Gln Leu Leu Lys Leu
 305                      310                      315                      320

Asn Ile Asp Ala Gly Gly Val Gln Ser Arg Arg Val Ile Asp Arg Ile
                      325                      330                      335

Leu Ala Ala Glu Gln Glu Ala Ala Asp Ala Ala Leu Ile Ala Arg Ser
                      340                      345                      350

Ala Ser

```

```

<210> 5
<211> 954
<212> DNA
<213> not required under old rule

```

```

<220>
<221> CDS
<222> (1)..(951)
<223> product = "Vanillin-O-Demethylase"/ gene = "vanB"

```

```

<400> 5
atg att gag gta atc att tcg gcg atg cgc ttg gtt gct cag gac atc 48
Met Ile Glu Val Ile Ile Ser Ala Met Arg Leu Val Ala Gln Asp Ile
  1           5           10           15

att agc ctt gag ttt gtc cgg gct gac ggt ggc ttg ctt ccg cct gtc 96
Ile Ser Leu Glu Phe Val Arg Ala Asp Gly Gly Leu Leu Pro Pro Val
          20           25           30

gag gcc ggc gcc cac gtc gat gtg cat ctt cct ggc ggc ctg att cgg 144
Glu Ala Gly Ala His Val Asp Val His Leu Pro Gly Gly Leu Ile Arg
          35           40           45

cag tac tcg ctc tgg aat caa cca ggg gcg cag agc cat tac tgc atc 192
Gln Tyr Ser Leu Trp Asn Gln Pro Gly Ala Gln Ser His Tyr Cys Ile
          50           55           60

ggg gtt ctg aag gac ccg gcg tct cgt ggt ggt tcg aag gcg gtg cac 240
Gly Val Leu Lys Asp Pro Ala Ser Arg Gly Gly Ser Lys Ala Val His
          65           70           75           80

gag aat ctt cgc gtc ggg atg cgc gtg caa att agc gag ccg agg aac 288
Glu Asn Leu Arg Val Gly Met Arg Val Gln Ile Ser Glu Pro Arg Asn
          85           90           95

cta ttc cca ttg gaa gag ggg gtg gag ccg agt ctg ctg ttc gcg ggc 336
Leu Phe Pro Leu Glu Glu Gly Val Glu Arg Ser Leu Leu Phe Ala Gly
          100           105           110

ggg att ggc att acg ccg att ctg tgt atg gct caa gaa tta gca gca 384
Gly Ile Gly Ile Thr Pro Ile Leu Cys Met Ala Gln Glu Leu Ala Ala
          115           120           125

cgc gag caa gat ttc gag ttg cat tat tgc gcg cgt tcg acc gac cga 432
Arg Glu Gln Asp Phe Glu Leu His Tyr Cys Ala Arg Ser Thr Asp Arg
          130           135           140

gcg gcg ttc gtt gaa tgg ctt aag gtt tgc gac ttt gct gat cac gta 480
Ala Ala Phe Val Glu Trp Leu Lys Val Cys Asp Phe Ala Asp His Val
          145           150           155           160

cgt ttc cac ttt gac aat ggc ccg gat cag caa aaa ctg aat gcc gca 528
Arg Phe His Phe Asp Asn Gly Pro Asp Gln Gln Lys Leu Asn Ala Ala
          165           170           175

gcg ctg cta gcg gcc gag gcc gaa ggt acc cac ctt tat gtc tgt ggg 576
Ala Leu Leu Ala Ala Glu Ala Glu Gly Thr His Leu Tyr Val Cys Gly
          180           185           190

ccc ggc ggg ttc atg ggg cat gtg ctt gat acc gcg aag gag cag ggc 624
Pro Gly Gly Phe Met Gly His Val Leu Asp Thr Ala Lys Glu Gln Gly
          195           200           205

tgg gct gac aat cga ctg cat cga gag tat ttc gcc gcg gcg ccg aat 672
Trp Ala Asp Asn Arg Leu His Arg Glu Tyr Phe Ala Ala Ala Pro Asn
          210           215           220

```



```

Arg Glu Gln Asp Phe Glu Leu His Tyr Cys Ala Arg Ser Thr Asp Arg
 130                      135                      140

Ala Ala Phe Val Glu Trp Leu Lys Val Cys Asp Phe Ala Asp His Val
 145                      150                      155                      160

Arg Phe His Phe Asp Asn Gly Pro Asp Gln Gln Lys Leu Asn Ala Ala
      165                      170                      175

Ala Leu Leu Ala Ala Glu Ala Glu Gly Thr His Leu Tyr Val Cys Gly
      180                      185                      190

Pro Gly Gly Phe Met Gly His Val Leu Asp Thr Ala Lys Glu Gln Gly
      195                      200                      205

Trp Ala Asp Asn Arg Leu His Arg Glu Tyr Phe Ala Ala Ala Pro Asn
      210                      215                      220

Val Ser Ala Asp Asp Gly Ser Phe Glu Val Arg Ile His Ser Thr Gly
      225                      230                      235                      240

Gln Val Leu Gln Val Pro Ala Asp Gln Thr Val Ser Gln Val Leu Asp
      245                      250                      255

Ala Ala Gly Ile Ile Val Pro Val Ser Cys Glu Gln Gly Ile Cys Gly
      260                      265                      270

Thr Cys Ile Thr Arg Val Val Asp Gly Glu Pro Asp His Arg Asp Phe
      275                      280                      285

Phe Leu Thr Asp Ala Glu Lys Ala Lys Asn Asp Gln Phe Thr Pro Cys
      290                      295                      300

Cys Ser Arg Ala Lys Ser Ala Cys Leu Val Leu Asp Leu
      305                      310                      315

```

```

<210> 7
<211> 1119
<212> DNA
<213> not required under old rule

<220>
<221> CDS
<222> (1)..(1116)
<223> product = "Formaldehyd-Dehydrogenase"/ gene =
      "fdh"

```

```

<400> 7
atg atc aaa tcc cgc gcc gct gtg gcg ttc gca ccc aat cag cca ttg      48
Met Ile Lys Ser Arg Ala Ala Val Ala Phe Ala Pro Asn Gln Pro Leu
  1                      5                      10                      15

cag atc gtc gaa gtg gac gtg gct ccg ccc aag gcc ggt gaa gtc ctg      96
Gln Ile Val Glu Val Asp Val Ala Pro Pro Lys Ala Gly Glu Val Leu
      20                      25                      30

```

gtg Val	cgg Arg	gtc Val	gtg Val	gcc Ala	acc Thr	ggc Gly	gtt Val	tgc Cys	cac His	acc Thr	gat Asp	gcc Ala	tac Tyr	acc Thr	ctg Leu	144
		35				40						45				
tcc Ser	ggc Gly	gct Ala	gat Asp	tcc Ser	gag Glu	ggc Gly	gtt Val	ttc Phe	ccc Pro	tgc Cys	atc Ile	ctt Leu	ggt Gly	cac His	gaa Glu	192
		50				55						60				
ggc Gly	ggc Gly	ggc Gly	att Ile	gtc Val	gaa Glu	gcg Ala	gtg Val	ggc Gly	gag Glu	ggc Gly	gtc Val	acc Thr	tcg Ser	ctg Leu	gcg Ala	240
		65				70						75				80
gtc Val	ggc Gly	gac Asp	cac His	gtg Val	atc Ile	ccg Pro	ctc Leu	tac Tyr	acg Thr	gcc Ala	gaa Glu	tgc Cys	cgt Arg	gag Glu	tgc Cys	288
				85						90				95		
aag Lys	ttc Phe	ttc Phe	aag Lys	tcc Ser	ggc Gly	aag Lys	acc Thr	aac Asn	ctg Leu	tgc Cys	cag Gln	aaa Lys	gtg Val	cgt Arg	gct Ala	336
				100				105						110		
act Thr	cag Gln	ggc Gly	aag Lys	ggc Gly	ctg Leu	atg Met	ccg Pro	gac Asp	ggc Gly	acc Thr	tcc Ser	cgc Arg	ttc Phe	agc Ser	tac Tyr	384
		115				120						125				
aac Asn	ggc Gly	cag Gln	ccg Pro	atc Ile	tac Tyr	cac His	tac Tyr	atg Met	ggc Gly	tgc Cys	tcg Ser	acc Thr	ttc Phe	tcc Ser	gag Glu	432
		130				135						140				
tac Tyr	acc Thr	gtg Val	ctg Leu	ccg Pro	gaa Glu	atc Ile	tcc Ser	ctg Leu	gcg Ala	aag Lys	att Ile	ccc Pro	aag Lys	aat Asn	gcg Ala	480
145						150				155						160
ccg Pro	ctg Leu	gag Glu	aaa Lys	gtc Val	tgc Cys	ctg Leu	ctg Leu	ggc Gly	tgc Cys	ggc Gly	gtg Val	acc Thr	acc Thr	ggc Gly	att Ile	528
				165				170						175		
ggc Gly	gcg Ala	gtg Val	ctg Leu	aac Asn	act Thr	gcc Ala	aag Lys	gtg Val	gag Glu	gag Glu	ggt Gly	gct Ala	acc Thr	gtg Val	gcc Ala	576
		180						185				190				
atc Ile	ttc Phe	ggc Gly	ctg Leu	ggc Gly	ggc Gly	atc Ile	ggc Gly	ttg Leu	gcg Ala	gcg Ala	atc Ile	atc Ile	ggc Gly	gcg Ala	aag Lys	624
		195				200						205				
atg Met	gcc Ala	aag Lys	gcc Ala	tcg Ser	cgc Arg	atc Ile	atc Ile	gcc Ala	atc Ile	gac Asp	atc Ile	aat Asn	ccg Pro	tcc Ser	aag Lys	672
		210				215						220				
ttc Phe	gat Asp	gtg Val	gct Ala	cgc Arg	gag Glu	ctg Leu	ggc Gly	gcc Ala	act Thr	gac Asp	ttc Phe	gtc Val	aat Asn	ccg Pro	aac Asn	720
225						230				235						240
gat Asp	cac His	gcg Ala	aag Lys	ccg Pro	atc Ile	cag Gln	gat Asp	gtc Val	atc Ile	gtc Val	gag Glu	atg Met	act Thr	gat Asp	ggc Gly	768
				245				250						255		

ggt	gtg	gac	tac	agc	ttc	gag	tgc	atc	ggc	aac	ggt	cga	ctc	atg	cgc	816
Gly	Val	Asp	Tyr	Ser	Phe	Glu	Cys	Ile	Gly	Asn	Val	Arg	Leu	Met	Arg	
		260						265					270			
gca	gca	ctc	gag	tgc	tgc	cac	aag	ggc	tgg	ggc	gaa	tcc	gtg	atc	atc	864
Ala	Ala	Leu	Glu	Cys	Cys	His	Lys	Gly	Trp	Gly	Glu	Ser	Val	Ile	Ile	
		275					280					285				
ggc	gtg	gcg	ccg	gcg	ggg	gcc	gaa	atc	aac	acc	cgt	ccg	ttc	cac	ctg	912
Gly	Val	Ala	Pro	Ala	Gly	Ala	Glu	Ile	Asn	Thr	Arg	Pro	Phe	His	Leu	
		290				295					300					
gtg	acc	ggt	cgc	gtc	tgg	cgg	ggt	tcg	gcg	ttc	ggt	ggc	gta	aag	ggc	960
Val	Thr	Gly	Arg	Val	Trp	Arg	Gly	Ser	Ala	Phe	Gly	Gly	Val	Lys	Gly	
305					310					315					320	
cgc	acc	gaa	ctg	ccg	agc	tac	gtg	gag	aag	gca	cag	cag	ggc	gag	atc	1008
Arg	Thr	Glu	Leu	Pro	Ser	Tyr	Val	Glu	Lys	Ala	Gln	Gln	Gly	Glu	Ile	
			325						330					335		
ccg	ctg	gac	acc	ttc	atc	act	cac	acc	atg	ggc	ctg	gac	gac	atc	aac	1056
Pro	Leu	Asp	Thr	Phe	Ile	Thr	His	Thr	Met	Gly	Leu	Asp	Asp	Ile	Asn	
			340					345					350			
acg	gcc	ttc	gac	ctg	atg	gac	gaa	ggg	aag	agc	atc	cgc	tct	gtt	gtt	1104
Thr	Ala	Phe	Asp	Leu	Met	Asp	Glu	Gly	Lys	Ser	Ile	Arg	Ser	Val	Val	
		355					360					365				
caa	ttg	agt	cgc	tag												1119
Gln	Leu	Ser	Arg													
	370															
<210> 8																
<211> 372																
<212> PRT																
<213> not required under old rule																
<400> 8																
Met	Ile	Lys	Ser	Arg	Ala	Ala	Val	Ala	Phe	Ala	Pro	Asn	Gln	Pro	Leu	
1				5					10					15		
Gln	Ile	Val	Glu	Val	Asp	Val	Ala	Pro	Pro	Lys	Ala	Gly	Glu	Val	Leu	
			20					25					30			
Val	Arg	Val	Val	Ala	Thr	Gly	Val	Cys	His	Thr	Asp	Ala	Tyr	Thr	Leu	
		35					40					45				
Ser	Gly	Ala	Asp	Ser	Glu	Gly	Val	Phe	Pro	Cys	Ile	Leu	Gly	His	Glu	
	50					55					60					
Gly	Gly	Gly	Ile	Val	Glu	Ala	Val	Gly	Glu	Gly	Val	Thr	Ser	Leu	Ala	
65					70					75					80	
Val	Gly	Asp	His	Val	Ile	Pro	Leu	Tyr	Thr	Ala	Glu	Cys	Arg	Glu	Cys	
				85					90					95		

Lys	Phe	Phe	Lys	Ser	Gly	Lys	Thr	Asn	Leu	Cys	Gln	Lys	Val	Arg	Ala
			100				105						110		
Thr	Gln	Gly	Lys	Gly	Leu	Met	Pro	Asp	Gly	Thr	Ser	Arg	Phe	Ser	Tyr
			115				120				125				
Asn	Gly	Gln	Pro	Ile	Tyr	His	Tyr	Met	Gly	Cys	Ser	Thr	Phe	Ser	Glu
			130				135				140				
Tyr	Thr	Val	Leu	Pro	Glu	Ile	Ser	Leu	Ala	Lys	Ile	Pro	Lys	Asn	Ala
145,				150						155			160		
Pro	Leu	Glu	Lys	Val	Cys	Leu	Leu	Gly	Cys	Gly	Val	Thr	Thr	Gly	Ile
			165						170			175			
Gly	Ala	Val	Leu	Asn	Thr	Ala	Lys	Val	Glu	Glu	Gly	Ala	Thr	Val	Ala
			180						185			190			
Ile	Phe	Gly	Leu	Gly	Gly	Ile	Gly	Leu	Ala	Ala	Ile	Ile	Gly	Ala	Lys
			195			200						205			
Met	Ala	Lys	Ala	Ser	Arg	Ile	Ile	Ala	Ile	Asp	Ile	Asn	Pro	Ser	Lys
			210			215			220						
Phe	Asp	Val	Ala	Arg	Glu	Leu	Gly	Ala	Thr	Asp	Phe	Val	Asn	Pro	Asn
225				230						235			240		
Asp	His	Ala	Lys	Pro	Ile	Gln	Asp	Val	Ile	Val	Glu	Met	Thr	Asp	Gly
			245						250			255			
Gly	Val	Asp	Tyr	Ser	Phe	Glu	Cys	Ile	Gly	Asn	Val	Arg	Leu	Met	Arg
			260			265						270			
Ala	Ala	Leu	Glu	Cys	Cys	His	Lys	Gly	Trp	Gly	Glu	Ser	Val	Ile	Ile
			275			280						285			
Gly	Val	Ala	Pro	Ala	Gly	Ala	Glu	Ile	Asn	Thr	Arg	Pro	Phe	His	Leu
			290			295			300						
Val	Thr	Gly	Arg	Val	Trp	Arg	Gly	Ser	Ala	Phe	Gly	Gly	Val	Lys	Gly
305				310						315			320		
Arg	Thr	Glu	Leu	Pro	Ser	Tyr	Val	Glu	Lys	Ala	Gln	Gln	Gly	Glu	Ile
			325						330			335			
Pro	Leu	Asp	Thr	Phe	Ile	Thr	His	Thr	Met	Gly	Leu	Asp	Asp	Ile	Asn
			340			345						350			
Thr	Ala	Phe	Asp	Leu	Met	Asp	Glu	Gly	Lys	Ser	Ile	Arg	Ser	Val	Val
			355			360						365			
Gln	Leu	Ser	Arg												
			370												

[illegible]

<221> CDS

```
<223> product = "gamma-Glutamylcystein-Synthetase" /  
gene = "gcs"
```

atg ccg caa act ctt gct gga cgg ttg agt ctg tta tcc ggc acc gac 48  
Met Pro Gln Thr Leu Ala Gly Arg Leu Ser Leu Leu Ser Gly Thr Asp  
1 5 10 15

gaa tta acc ctg ctt ctt cgg ggt ggt cgg ggc att gag cgt gaa gcc 96  
Glu Leu Thr Leu Leu Leu Arg Gly Gly Arg Gly Ile Glu Arg Glu Ala  
20 25 30

ttg cgg gtc gat gtt caa ggt gaa ctg gcg ctg acg cct cac ccg gcg 144  
Leu Arg Val Asp Val Gln Gly Glu Leu Ala Leu Thr Pro His Pro Ala  
35 40 45

gcg ctt ggc tct gcg ttg acc cat ccg aca att act acg gat tac gcc 192  
Ala Leu Gly Ser Ala Leu Thr His Pro Thr Ile Thr Thr Asp Tyr Ala  
50 55 60

gag gcc ctg ctt gag ttg atc act cgg ccg gca acc gat tgt gcg caa 240  
Glu Ala Leu Leu Glu Leu Ile Thr Arg Pro Ala Thr Asp Cys Ala Gln  
65 70 75 80

gcc ttg gct gag ctg gag gag ctt cac cgt ttc gtt cat tcg aga ctt 288  
Ala Leu Ala Glu Leu Glu Glu Leu His Arg Phe Val His Ser Arg Leu  
85 90 95

gag ggg gag tat ctc tgg aat ctg tcc atg cct ggc aga ttg ccg gtt 336  
Glu Gly Glu Tyr Leu Trp Asn Leu Ser Met Pro Gly Arg Leu Pro Val  
100 105 110

gat gag caa atc ccg att gct tgg tat gga cca tca aat cca ggc atg 384  
Asp Glu Gln Ile Pro Ile Ala Trp Tyr Gly Pro Ser Asn Pro Gly Met  
115 120 125

ttg	cgc	cac	gtt	tat	cgc	cgt	ggc	cta	gct	ctg	cgt	tat	ggc	aag	cga	432
Leu	Arg	His	Val	Tyr	Arg	Arg	Gly	Leu	Ala	Leu	Arg	Tyr	Gly	Lys	Arg	
	130					135					140					

atg caa tgc atc gca ggg att cac tac aac tac tca ctg ccg cca gag 480  
Met Gln Cys Ile Ala Gly Ile His Tyr Asn Tyr Ser Leu Pro Pro Glu  
145 150 155 160

ctt ttc gct gtc ctg acc aag gca gag gtc ggg tct ccc aag tta ctg 528  
Leu Phe Ala Val Leu Thr Lys Ala Glu Val Gly Ser Pro Lys Leu Leu  
165 170 175



gag Glu	cgc Arg	cag Gln	tca Ser 180	gca Ala	gct Ala	tac Tyr	atg Met	cgc Arg 185	caa Gln	att Ile	cgc Arg	aac Asn	ctt Leu 190	cgg Arg	caa Gln	576
tac Tyr	ggt Gly	tgg Trp 195	ttg Leu	ctg Leu	gcc Ala	tac Tyr	ttg Leu 200	ttc Phe	ggc Gly	gct Ala	tcc Ser	ccc Pro 205	gcc Ala	atc Ile	tgc Cys	624
aag Lys	agc Ser	ttc Phe 210	ttg Leu	ggg Gly	ggc Gly	gag Glu 215	aga Arg	gat Asp	gag Glu	cta Leu	gct Ala 220	cgc Arg	atg Met	ggg Gly	ggc Gly	672
gat Asp 225	acg Thr	ctt Leu	tac Tyr	atg Met	ccc Pro 230	tat Tyr	gca Ala	acc Thr	agc Ser	ttg Leu 235	cgc Arg	atg Met	agt Ser	gac Asp	atc Ile 240	720
ggg Gly	tac Tyr	cgc Arg	aac Asn 245	cgt Arg	gcc Ala	atg Met	gat Asp	gat Asp 250	cta Leu	tct Ser	ccc Pro	agc Ser	ctg Leu	aat Asn 255	gat Asp	768
ctg Leu	ggt Gly	gcc Ala	tat Tyr 260	att Ile	cgc Arg	gat Asp	att Ile 265	tgc Cys 265	cgt Arg	gct Ala	ctt Leu	cac His	act Thr 270	ccc Pro	gat Asp	816
gcc Ala	cag Gln 275	tac Tyr	cag Gln	gcg Ala	ctg Leu	ggt Gly	gtg Val 280	ttt Phe	gca Ala	cag Gln	ggc Gly 285	gag Glu	tgg Trp	cgg Arg	cag Gln	864
tta Leu 290	aac Asn	gcc Ala	aat Asn	cta Leu	ttg Leu	cag Gln 295	ttg Leu	gat Asp	agt Ser	gag Glu 300	tac Tyr	tac Tyr	gca Ala	ctg Leu	gcg Ala	912
cga Arg 305	ccg Pro	aag Lys	tca Ser	gcg Ala	ccc Pro 310	gag Glu	cgg Arg	ggg Gly	gag Glu	cga Arg 315	aac Asn	ctg Leu	gat Asp	gct Ala	ctc Leu 320	960
gct Ala	agg Arg	cgt Arg	gga Gly	gtc Val 325	cag Gln	tat Tyr	gtg Val	gag Glu 330	ctg Leu	cgc Arg	gca Ala	ctg Leu	gat Asp	ctc Leu 335	gat Asp	1008
cca Pro	ttc Phe	tcc Ser	ccg Pro 340	tta Leu	ggc Gly	att Ile	ggc Gly	ctg Leu 345	acc Thr	tgc Cys	gcc Ala	aag Lys	ttc Phe 350	ctc Leu	gat Asp	1056
ggc Gly	ttt Phe 355	ttg Leu	ctt Leu	ttc Phe	tgc Cys	ttg Leu	ttg Leu 360	tct Ser	gag Glu	gcg Ala	ccg Pro 365	gtt Val	gat Asp	gat Asp	cga Arg	1104
aat Asn 370	gcc Ala	cag Gln	cgt Arg	tca Ser	aga Arg	ccg Pro 375	gga Gly	aaa Lys	tct Ser	gag Glu 380	cct Pro	ggc Gly	cgg Arg	caa Gln	gta Val	1152
cgg Arg 385	gcg Ala	tca Ser	cct Pro	ggc Gly	tta Leu 390	aag Lys	ctg Leu	cat His	cgg Arg 395	aat Asn	ggg Gly	cag Gln	tcc Ser	att Ile	ctc Leu 400	1200

[illegible]

```
<210> 10
<211> 545
<212> PRT
<213> not required under old rule
```

```

<400> 10
Met  Pro  Gln  Thr  Leu  Ala  Gly  Arg  Leu  Ser  Leu  Leu  Ser  Gly  Thr  Asp
  1              5              10              15

Glu  Leu  Thr  Leu  Leu  Leu  Arg  Gly  Gly  Arg  Gly  Ile  Glu  Arg  Glu  Ala
      20              25              30

Leu  Arg  Val  Asp  Val  Gln  Gly  Glu  Leu  Ala  Leu  Thr  Pro  His  Pro  Ala
      35              40              45

```

Ala	Leu	Gly	Ser	Ala	Leu	Thr	His	Pro	Thr	Ile	Thr	Thr	Asp	Tyr	Ala
50						55					60				
Glu	Ala	Leu	Leu	Glu	Leu	Ile	Thr	Arg	Pro	Ala	Thr	Asp	Cys	Ala	Gln
65					70					75					80
Ala	Leu	Ala	Glu	Leu	Glu	Glu	Leu	His	Arg	Phe	Val	His	Ser	Arg	Leu
				85				90						95	
Glu	Gly	Glu	Tyr	Leu	Trp	Asn	Leu	Ser	Met	Pro	Gly	Arg	Leu	Pro	Val
			100					105					110		
Asp	Glu	Gln	Ile	Pro	Ile	Ala	Trp	Tyr	Gly	Pro	Ser	Asn	Pro	Gly	Met
		115				120						125			
Leu	Arg	His	Val	Tyr	Arg	Arg	Gly	Leu	Ala	Leu	Arg	Tyr	Gly	Lys	Arg
	130				135						140				
Met	Gln	Cys	Ile	Ala	Gly	Ile	His	Tyr	Asn	Tyr	Ser	Leu	Pro	Pro	Glu
145					150					155					160
Leu	Phe	Ala	Val	Leu	Thr	Lys	Ala	Glu	Val	Gly	Ser	Pro	Lys	Leu	Leu
				165					170					175	
Glu	Arg	Gln	Ser	Ala	Ala	Tyr	Met	Arg	Gln	Ile	Arg	Asn	Leu	Arg	Gln
			180					185					190		
Tyr	Gly	Trp	Leu	Leu	Ala	Tyr	Leu	Phe	Gly	Ala	Ser	Pro	Ala	Ile	Cys
		195					200					205			
Lys	Ser	Phe	Leu	Gly	Gly	Glu	Arg	Asp	Glu	Leu	Ala	Arg	Met	Gly	Gly
	210				215						220				
Asp	Thr	Leu	Tyr	Met	Pro	Tyr	Ala	Thr	Ser	Leu	Arg	Met	Ser	Asp	Ile
225					230					235					240
Gly	Tyr	Arg	Asn	Arg	Ala	Met	Asp	Asp	Leu	Ser	Pro	Ser	Leu	Asn	Asp
				245					250					255	
Leu	Gly	Ala	Tyr	Ile	Arg	Asp	Ile	Cys	Arg	Ala	Leu	His	Thr	Pro	Asp
			260					265					270		
Ala	Gln	Tyr	Gln	Ala	Leu	Gly	Val	Phe	Ala	Gln	Gly	Glu	Trp	Arg	Gln
		275					280					285			
Leu	Asn	Ala	Asn	Leu	Leu	Gln	Leu	Asp	Ser	Glu	Tyr	Tyr	Ala	Leu	Ala
	290					295					300				
Arg	Pro	Lys	Ser	Ala	Pro	Glu	Arg	Gly	Glu	Arg	Asn	Leu	Asp	Ala	Leu
305					310					315					320
Ala	Arg	Arg	Gly	Val	Gln	Tyr	Val	Glu	Leu	Arg	Ala	Leu	Asp	Leu	Asp
				325					330					335	
Pro	Phe	Ser	Pro	Leu	Gly	Ile	Gly	Leu	Thr	Cys	Ala	Lys	Phe	Leu	Asp
			340					345					350		



```

ttc atc tct cag gga gct tgg gca gag agc ccc gca gcc tct ggc aat 96
Phe Ile Ser Gln Gly Ala Trp Ala Glu Ser Pro Ala Ala Ser Gly Asn
      20                      25                      30

acc cct gac att tat cga aag acc tgc acc tac tgc cat gag cct act 144
Thr Pro Asp Ile Tyr Arg Lys Thr Cys Thr Tyr Cys His Glu Pro Thr
      35                      40                      45

gtc aac aat ggc cgg gtc att gcc cga agc ctc ggg ccg act ctg cga 192
Val Asn Asn Gly Arg Val Ile Ala Arg Ser Leu Gly Pro Thr Leu Arg
      50                      55                      60

ggg cgc cag atc cct cca cag tac acg gag tac atg gtg cgt cat gga 240
Gly Arg Gln Ile Pro Pro Gln Tyr Thr Glu Tyr Met Val Arg His Gly
      65                      70                      75                      80

cgc ggg gca atg cct gca ttc tct gaa gca gaa gtg cct ccg gcg gag 288
Arg Gly Ala Met Pro Ala Phe Ser Glu Ala Glu Val Pro Pro Ala Glu
      85                      90                      95

ctg aaa gtt ctg ggc gat tgg att cag caa agc agt gct ccc aaa gac 336
Leu Lys Val Leu Gly Asp Trp Ile Gln Gln Ser Ser Ala Pro Lys Asp
      100                      105                      110

gct gga gtc gcg cca tga 354
Ala Gly Val Ala Pro
      115

<210> 12
<211> 117
<212> PRT
<213> not required under old rule

<400> 12
Met Met Asn Val Asn Tyr Lys Ala Val Gly Ala Ser Leu Leu Leu Ala
  1                      5                      10                      15

Phe Ile Ser Gln Gly Ala Trp Ala Glu Ser Pro Ala Ala Ser Gly Asn
      20                      25                      30

Thr Pro Asp Ile Tyr Arg Lys Thr Cys Thr Tyr Cys His Glu Pro Thr
      35                      40                      45

Val Asn Asn Gly Arg Val Ile Ala Arg Ser Leu Gly Pro Thr Leu Arg
      50                      55                      60

Gly Arg Gln Ile Pro Pro Gln Tyr Thr Glu Tyr Met Val Arg His Gly
      65                      70                      75                      80

Arg Gly Ala Met Pro Ala Phe Ser Glu Ala Glu Val Pro Pro Ala Glu
      85                      90                      95

Leu Lys Val Leu Gly Asp Trp Ile Gln Gln Ser Ser Ala Pro Lys Asp
      100                      105                      110

```

Ala Gly Val Ala Pro  
115

<210> 13  
<211> 687  
<212> DNA  
<213> not required under old rule

<220>  
<221> CDS  
<222> (1) .. (684)  
<223> gene = "ORF5"

<400> 13  
atg act acc cgt cgc aac ttt cta ata ggc gcg tcg cag gtg ggg gca 48  
Met Thr Thr Arg Arg Asn Phe Leu Ile Gly Ala Ser Gln Val Gly Ala  
1 5 10 15  
ttg gtg atg atg tcg ccg aaa ttg gtc ttc cgt acg ccg ctc aag cag 96  
Leu Val Met Met Ser Pro Lys Leu Val Phe Arg Thr Pro Leu Lys Gln  
20 25 30  
aag ccc gtg cgc atc ctg tcg acc ggg ctg gcc ggt gag caa gag ttt 144  
Lys Pro Val Arg Ile Leu Ser Thr Gly Leu Ala Gly Glu Gln Glu Phe  
35 40 45  
cac tcg atg ctt cgc gcg cga ttg acc cat acg ggt cag gtc gac atc 192  
His Ser Met Leu Arg Ala Arg Leu Thr His Thr Gly Gln Val Asp Ile  
50 55 60  
gcg tcg gta ccg ctg gac gca gct att tgg gct tct ccc gct cga ctt 240  
Ala Ser Val Pro Leu Asp Ala Ala Ile Trp Ala Ser Pro Ala Arg Leu  
65 70 75 80  
gcc cag gca atg gat gcg ttg aat ggt acg cgt ctg atc gct ttt gtt 288  
Ala Gln Ala Met Asp Ala Leu Asn Gly Thr Arg Leu Ile Ala Phe Val  
85 90 95  
gag ccc agg aac gaa ttg ata ctg atg caa ttc ttg atg gat cgc ggg 336  
Glu Pro Arg Asn Glu Leu Ile Leu Met Gln Phe Leu Met Asp Arg Gly  
100 105 110  
gct gcg gtg ctt att caa ggt gag cat gcg gtg gac agc aag ggg gtc 384  
Ala Ala Val Leu Ile Gln Gly Glu His Ala Val Asp Ser Lys Gly Val  
115 120 125  
tct cgg cac gac ttt ctg agt acc cca tcc agt gcg gga att gga ggg 432  
Ser Arg His Asp Phe Leu Ser Thr Pro Ser Ser Ala Gly Ile Gly Gly  
130 135 140  
gcg cta gcc gac agc ctg gca aaa ggg ggc tcg ccg ttc tct att tcc 480  
Ala Leu Ala Asp Ser Leu Ala Lys Gly Gly Ser Pro Phe Ser Ile Ser  
145 150 155 160







aac aag atc att gag atc gat gtt gag ggg tgt act gcc ctg ctc gag	384
Asn Lys Ile Ile Glu Ile Asp Val Glu Gly Cys Thr Ala Leu Leu Glu	
115 120 125	
ccg ggc gtt acc tac cag cag ctt cac gat tac atc aag gag cac aat	432
Pro Gly Val Thr Tyr Gln Gln Leu His Asp Tyr Ile Lys Glu His Asn	
130 135 140	
ctg ccc ttg atg ctg gat gtg ccg act att ggg cct atg gtt ggc ccg	480
Leu Pro Leu Met Leu Asp Val Pro Thr Ile Gly Pro Met Val Gly Pro	
145 150 155 160	
gtg ggt aac acg ctg gat cga ggc gtt ggt tat acg ccg tac ggc gag	528
Val Gly Asn Thr Leu Asp Arg Gly Val Gly Tyr Thr Pro Tyr Gly Glu	
165 170 175	
cac ttc atg atg cag tgt ggt atg gaa gtc gtc atg gcc gat ggc gaa	576
His Phe Met Met Gln Cys Gly Met Glu Val Val Met Ala Asp Gly Glu	
180 185 190	
atc ctc cgt act ggt atg ggc tcg gtg ccc aaa gcc aag act tgg cag	624
Ile Leu Arg Thr Gly Met Gly Ser Val Pro Lys Ala Lys Thr Trp Gln	
195 200 205	
gca ttc aaa tgg ggc tat ggt cca tat ctg gac ggt atc ttt acc cag	672
Ala Phe Lys Trp Gly Tyr Gly Pro Tyr Leu Asp Gly Ile Phe Thr Gln	
210 215 220	
tcc aac ttt ggt gtt gtg aca aag ctc ggg att tgg ttg atg ccc aag	720
Ser Asn Phe Gly Val Val Thr Lys Leu Gly Ile Trp Leu Met Pro Lys	
225 230 235 240	
ccg cca gtg atc aag tcg ttt atg atc cgt tat ccc aat gaa gct gat	768
Pro Pro Val Ile Lys Ser Phe Met Ile Arg Tyr Pro Asn Glu Ala Asp	
245 250 255	
gtg gtt aag gca att gat gct ttt cgc ccg ctg cgt att act cag ctg	816
Val Val Lys Ala Ile Asp Ala Phe Arg Pro Leu Arg Ile Thr Gln Leu	
260 265 270	
att cct aac gtc gtt ttg ttc atg cac ggc atg tac gaa acg gca atc	864
Ile Pro Asn Val Val Leu Phe Met His Gly Met Tyr Glu Thr Ala Ile	
275 280 285	
tgc cgg acg cgt gct gag gtt act tcg gac cca ggt cct att tct gaa	912
Cys Arg Thr Arg Ala Glu Val Thr Ser Asp Pro Gly Pro Ile Ser Glu	
290 295 300	
gcg gac gcc cgc aaa gca ttc aaa gag cta ggc gtt ggc tac tgg aac	960
Ala Asp Ala Arg Lys Ala Phe Lys Glu Leu Gly Val Gly Tyr Trp Asn	
305 310 315 320	
gtt tac ttc gcg ctt tac ggc aca gaa gag cag ata gcc gtc aat gaa	1008
Val Tyr Phe Ala Leu Tyr Gly Thr Glu Glu Gln Ile Ala Val Asn Glu	
325 330 335	

aag atc gtc cgc ggc atc ctc gaa ccg acg ggg ggt gag atc ctc acc	1056
Lys Ile Val Arg Gly Ile Leu Glu Pro Thr Gly Gly Glu Ile Leu Thr	
340 345 350	
gaa gag gag gct gga gat aac att ctt ttc cat cac cat aag cag ctc	1104
Glu Glu Glu Ala Gly Asp Asn Ile Leu Phe His His His Lys Gln Leu	
355 360 365	
atg aac ggc gag atg aca ttg gag gaa atg aat atc tac cag tgg cgc	1152
Met Asn Gly Glu Met Thr Leu Glu Glu Met Asn Ile Tyr Gln Trp Arg	
370 375 380	
gga gca ggt ggc ggt gct tgc tgg ttt gca ccg gtt gct cag gtc aag	1200
Gly Ala Gly Gly Gly Ala Cys Trp Phe Ala Pro Val Ala Gln Val Lys	
385 390 395 400	
ggg cat gag gca gag cag cag gtc aag ctt gct cag aag gtg ctt gca	1248
Gly His Glu Ala Glu Gln Gln Val Lys Leu Ala Gln Lys Val Leu Ala	
405 410 415	
aag cat ggg ttc gat tac acg gcg ggc ttt gcg att ggt tgg cgc gat	1296
Lys His Gly Phe Asp Tyr Thr Ala Gly Phe Ala Ile Gly Trp Arg Asp	
420 425 430	
ctt cac cat gtg atc gat gtg ctg tac gac cgt agc aat gcc gac gag	1344
Leu His His Val Ile Asp Val Leu Tyr Asp Arg Ser Asn Ala Asp Glu	
435 440 445	
aaa aag cgc gct tac gct tgc ttt gat gaa ttg atc gac gtc ttt gcg	1392
Lys Lys Arg Ala Tyr Ala Cys Phe Asp Glu Leu Ile Asp Val Phe Ala	
450 455 460	
gcc gaa ggc ttt gca agt tac agg acc aat att gcc ttt atg gac aaa	1440
Ala Glu Gly Phe Ala Ser Tyr Arg Thr Asn Ile Ala Phe Met Asp Lys	
465 470 475 480	
gtc gcc tct aag ttc ggc gct gag aat aag agg gtc aat cag aag atc	1488
Val Ala Ser Lys Phe Gly Ala Glu Asn Lys Arg Val Asn Gln Lys Ile	
485 490 495	
aag gct gcc ctt gat cca aac ggc atc atc gct ccc ggc aag tcg ggc	1536
Lys Ala Ala Leu Asp Pro Asn Gly Ile Ile Ala Pro Gly Lys Ser Gly	
500 505 510	
att cat ctt ccc aaa taa	1554
Ile His Leu Pro Lys	
515	

<210> 16

<211> 517

<212> PRT

<213> not required under old rule

<400> 16

Met	Glu	Ser	Thr	Val	Val	Leu	Pro	Glu	Gly	Val	Thr	Pro	Glu	Gln	Phe
1					5				10					15	

Thr	Lys	Ala	Ile	Ser	Glu	Phe	Arg	Gln	Val	Leu	Gly	Glu	Asp	Ser	Val			
			20				25						30					
Leu	Val	Thr	Ala	Glu	Arg	Val	Val	Pro	Tyr	Thr	Lys	Leu	Leu	Ile	Pro			
			35				40						45					
Thr	Gln	Asp	Asp	Ala	Gln	Tyr	Thr	Pro	Ala	Gly	Ala	Leu	Thr	Pro	Ser			
			50				55						60					
Ser	Val	Glu	Gln	Val	Gln	Lys	Val	Met	Gly	Ile	Cys	Asn	Lys	Tyr	Lys			
			65				70						75	80				
Ile	Pro	Val	Trp	Pro	Ile	Ser	Thr	Gly	Arg	Asn	Trp	Gly	Tyr	Gly	Ser			
			85						90						95			
Ala	Ser	Pro	Ala	Thr	Pro	Gly	Gln	Met	Ile	Leu	Asp	Leu	Arg	Lys	Met			
			100						105						110			
Asn	Lys	Ile	Ile	Glu	Ile	Asp	Val	Glu	Gly	Cys	Thr	Ala	Leu	Leu	Glu			
			115						120						125			
Pro	Gly	Val	Thr	Tyr	Gln	Gln	Leu	His	Asp	Tyr	Ile	Lys	Glu	His	Asn			
			130						135						140			
Leu	Pro	Leu	Met	Leu	Asp	Val	Pro	Thr	Ile	Gly	Pro	Met	Val	Gly	Pro			
			145						150						155	160		
Val	Gly	Asn	Thr	Leu	Asp	Arg	Gly	Val	Gly	Tyr	Thr	Pro	Tyr	Gly	Glu			
			165						170						175			
His	Phe	Met	Met	Gln	Cys	Gly	Met	Glu	Val	Val	Met	Ala	Asp	Gly	Glu			
			180						185						190			
Ile	Leu	Arg	Thr	Gly	Met	Gly	Ser	Val	Pro	Lys	Ala	Lys	Thr	Trp	Gln			
			195						200						205			
Ala	Phe	Lys	Trp	Gly	Tyr	Gly	Pro	Tyr	Leu	Asp	Gly	Ile	Phe	Thr	Gln			
			210						215						220			
Ser	Asn	Phe	Gly	Val	Val	Thr	Lys	Leu	Gly	Ile	Trp	Leu	Met	Pro	Lys			
			225						230						235	240		
Pro	Pro	Val	Ile	Lys	Ser	Phe	Met	Ile	Arg	Tyr	Pro	Asn	Glu	Ala	Asp			
			245						250						255			
Val	Val	Lys	Ala	Ile	Asp	Ala	Phe	Arg	Pro	Leu	Arg	Ile	Thr	Gln	Leu			
			260						265						270			
Ile	Pro	Asn	Val	Val	Leu	Phe	Met	His	Gly	Met	Tyr	Glu	Thr	Ala	Ile			
			275						280						285			
Cys	Arg	Thr	Arg	Ala	Glu	Val	Thr	Ser	Asp	Pro	Gly	Pro	Ile	Ser	Glu			
			290						295						300			
Ala	Asp	Ala	Arg	Lys	Ala	Phe	Lys	Glu	Leu	Gly	Val	Gly	Tyr	Trp	Asn			
			305						310						315	320		



gag Glu	cga Arg	cta Leu	ggg Gly 20	gac Asp	tgc Cys	ggt Gly	ctt Leu	atc Ile	ggt Gly	caa Gln	gtt Val	cga Arg	ttg Leu	acg Thr	gct Ala	96
cgc Arg	gat Asp	cct Pro 35	aaa Lys	agg Arg	ctt Leu	cgt Arg	gcc Ala	gct Ala	gcc Ala	gag Glu	gaa Glu	ggg Gly 45	ttt Phe	cag Gln	gtc Val	144
gct Ala	aag Lys 50	gcg Ala	gat Asp	tac Tyr	gcc Ala	gat Asp	att Ile	ggg Gly	agt Ser	ctt Leu	gac Asp	cag Gln	gca Ala	tta Leu	cag Gln	192
ggg Gly 65	gta Val	gac Asp	gta Val	tta Leu	ctc Leu 70	ctg Leu	att Ile	tct Ser	ggt Gly	act Thr 75	gca Ala	ccc Pro	aat Asn	gaa Glu	ata Ile 80	240
agg Arg	atc Ile	caa Gln	cag Gln	cat His 85	aag Lys	tcg Ser	gtc Val	atc Ile	gac Asp 90	gcg Ala	gca Ala	aaa Lys	cga Arg	aac Asn	ggc Gly 95	288
gtg Val	tcg Ser	cgt Arg	att Ile	gtg Val	tat Tyr	acc Thr	agc Ser	ttc Phe	ata Ile	aat Asn	cca Pro	agt Ser	act Thr	cgc Arg	agc Ser	336
agg Arg	tct Ser	att Ile 115	tgg Trp	gcc Ala	tcc Ser	att Ile	cat His	cgt Arg	gaa Glu	act Thr	gag Glu	act Thr	tac Tyr	ctc Leu	agg Arg	384
cag Gln	tct Ser	ggg Gly	gtg Val	aag Lys	ttt Phe	acg Thr	att Ile	gtc Val	cga Arg	aat Asn	aat Asn	cag Gln	tat Tyr	gcg Ala	tct Ser	432
aac Asn 145	ctg Leu	gat Asp	ctg Leu	ttg Leu	ctg Leu 150	ctg Leu	agg Arg	gct Ala	caa Gln	gac Asp 155	agc Ser	gga Gly	ata Ile	ttt Phe	gcc Ala 160	480
att Ile	ccc Pro	ggg Gly	gcg Ala	aag Lys 165	ggg Gly	cgg Arg	gtg Val	gcg Ala	tac Tyr 170	gtc Val	tct Ser	cat His	cgc Arg	gac Asp	gtt Val 175	528
gcc Ala	gct Ala	gcc Ala	atc Ile	tgt Cys	agt Ser	gtc Val	ctg Leu	acg Thr	acc Thr	gcc Ala	gga Gly	cac His	gat Asp	aac Asn	agg Arg	576
atc Ile	tac Tyr	cag Gln	ctc Leu	aca Thr	ggc Gly	tct Ser	gag Glu	gct Ala	ctc Leu	aat Asn	ggg Gly	ctc Leu	gag Glu	atc Ile	gcg Ala	624
gag Glu	att Ile	ctt Leu	ggt Gly	ggg Gly	gtg Val	ctc Leu	ggg Gly	cgt Arg	cca Pro	gtg Val	cgc Arg	gcg Ala	atg Met	gat Asp	gcc Ala	672
tcg Ser 225	cct Pro	gac Asp	gag Glu	ttt Phe	gct Ala	gcc Ala	agc Ser	ttt Phe	cgc Arg	gag Glu	gct Ala	gga Gly	ttc Phe	cct Pro	gag Glu 240	720

ttt atg gtt gaa ggc cta cta agc att tat gcc gct tca ggt gct ggg 768  
Phe Met Val Glu Gly Leu Leu Ser Ile Tyr Ala Ala Ser Gly Ala Gly  
245 250 255

gag tac caa tcc gtc agt cct gat gtt ggg ttg ttg acg gga cga cgt 816  
Glu Tyr Gln Ser Val Ser Pro Asp Val Gly Leu Leu Thr Gly Arg Arg  
260 265 270

gcc gaa tcg atg cga act tac ata cag cgt cta gtt tgg cct tga 861  
Ala Glu Ser Met Arg Thr Tyr Ile Gln Arg Leu Val Trp Pro  
275 280 285

<210> 18

<211> 286

<212> PRT

<213> not required under old rule

<400> 18

Met Ile Ala Ile Thr Ala Gly Thr Gly Ser Leu Gly Arg Ala Ile Val  
1 5 10 15

Glu Arg Leu Gly Asp Cys Gly Leu Ile Gly Gln Val Arg Leu Thr Ala  
20 25 30

Arg Asp Pro Lys Arg Leu Arg Ala Ala Ala Glu Glu Gly Phe Gln Val  
35 40 45

Ala Lys Ala Asp Tyr Ala Asp Ile Gly Ser Leu Asp Gln Ala Leu Gln  
50 55 60

Gly Val Asp Val Leu Leu Leu Ile Ser Gly Thr Ala Pro Asn Glu Ile  
65 70 75 80

Arg Ile Gln Gln His Lys Ser Val Ile Asp Ala Ala Lys Arg Asn Gly  
85 90 95

Val Ser Arg Ile Val Tyr Thr Ser Phe Ile Asn Pro Ser Thr Arg Ser  
100 105 110

Arg Ser Ile Trp Ala Ser Ile His Arg Glu Thr Glu Thr Tyr Leu Arg  
115 120 125

Gln Ser Gly Val Lys Phe Thr Ile Val Arg Asn Asn Gln Tyr Ala Ser  
130 135 140

Asn Leu Asp Leu Leu Leu Leu Arg Ala Gln Asp Ser Gly Ile Phe Ala  
145 150 155 160

Ile Pro Gly Ala Lys Gly Arg Val Ala Tyr Val Ser His Arg Asp Val  
165 170 175

Ala Ala Ala Ile Cys Ser Val Leu Thr Thr Ala Gly His Asp Asn Arg  
180 185 190

Ile Tyr Gln Leu Thr Gly Ser Glu Ala Leu Asn Gly Leu Glu Ile Ala  
195 200 205

Glu Ile Leu Gly Gly Val Leu Gly Arg Pro Val Arg Ala Met Asp Ala  
 210 215 220

Ser Pro Asp Glu Phe Ala Ala Ser Phe Arg Glu Ala Gly Phe Pro Glu  
 225 230 235 240

Phe Met Val Glu Gly Leu Leu Ser Ile Tyr Ala Ala Ser Gly Ala Gly  
 245 250 255

Glu Tyr Gln Ser Val Ser Pro Asp Val Gly Leu Leu Thr Gly Arg Arg  
 260 265 270

Ala Glu Ser Met Arg Thr Tyr Ile Gln Arg Leu Val Trp Pro  
 275 280 285

<210> 19  
 <211> 1011  
 <212> DNA  
 <213> not required under old rule

<220>  
 <221> CDS  
 <222> (1)..(1008)  
 <223> product = "Alkohol-Dehydrogenase" / gene = "adh"

<400> 19  
 atg aag gct tat gag ctt cac aag att tcg gaa cag gta gag gtc agg 48  
 Met Lys Ala Tyr Glu Leu His Lys Ile Ser Glu Gln Val Glu Val Arg  
 1 5 10 15

ctc cag cca act cgg ccc cgc ccg cag ttg aat cat ggc gag gtc ctc 96  
 Leu Gln Pro Thr Arg Pro Arg Pro Gln Leu Asn His Gly Glu Val Leu  
 20 25 30

atc agg gtc cat gca gcc tcg ctc aac ttt cgc gat ttg atg atc ttg 144  
 Ile Arg Val His Ala Ala Ser Leu Asn Phe Arg Asp Leu Met Ile Leu  
 35 40 45

gcc ggt cgc tat ccg ggt caa atg aaa ccc gat gtg atc ccg ctg tcc 192  
 Ala Gly Arg Tyr Pro Gly Gln Met Lys Pro Asp Val Ile Pro Leu Ser  
 50 55 60

gat ggt gct ggc gag att gtg gag gtc ggg cct ggc gta tct tcg gag 240  
 Asp Gly Ala Gly Glu Ile Val Glu Val Gly Pro Gly Val Ser Ser Glu  
 65 70 75 80

gtg cag ggt cag cgc gta gcc agc acc ttt ttc cct aac tgg cgg gcc 288  
 Val Gln Gly Gln Arg Val Ala Ser Thr Phe Phe Pro Asn Trp Arg Ala  
 85 90 95

gga aag att acc gag ccg gct att gag gtg tcg ttg ggc ttc ggt atg 336  
 Gly Lys Ile Thr Glu Pro Ala Ile Glu Val Ser Leu Gly Phe Gly Met  
 100 105 110

gac Asp	ggg Gly	atg Met	ctc Leu	gcg Ala	gaa Glu	tac Tyr	gtt Val	gct Ala	ctg Leu	ccc Pro	tat Tyr	gag Glu	gca Ala	acg Thr	ata Ile	384
115120125																
ccg Pro	ata Ile	ccg Pro	gag Glu	cac His	ctg Leu	tcg Ser	tac Tyr	gag Glu	gag Glu	gct Ala	gca Ala	aca Thr	ttg Leu	cct Pro	tgc Cys	432
130135140																
gcg Ala	gcg Ala	cta Leu	acc Thr	gct Ala	tgg Trp	aat Asn	gcg Ala	ttg Leu	acc Thr	gaa Glu	gtg Val	ggg Gly	cgt Arg	gtc Val	aag Lys	480
145150155160																
gcc Ala	ggt Gly	gat Asp	acg Thr	gtc Val	ttg Leu	ttg Leu	ctt Leu	ggc Gly	act Thr	ggc Gly	ggt Gly	gtc Val	tcg Ser	atg Met	ttc Phe	528
165170175																
gcg Ala	ttg Leu	cag Gln	ttc Phe	gcc Ala	aag Lys	ctc Leu	ttg Leu	ggg Gly	gcg Ala	acg Thr	gtc Val	att Ile	cac His	acc Thr	tcg Ser	576
180185190																
agc Ser	agt Ser	gaa Glu	caa Gln	aag Lys	ctg Leu	gag Glu	agg Arg	gtg Val	aaa Lys	gcg Ala	atg Met	ggg Gly	gct Ala	gat Asp	cat His	624
195200205																
ctg Leu	atc Ile	aac Asn	tac Tyr	cgc Arg	aat Asn	tcg Ser	cca Pro	ggg Gly	tgg Trp	gac Asp	cgt Arg	act Thr	gtc Val	ctg Leu	gat Asp	672
210215220																
ctc Leu	acc Thr	gcg Ala	ggg Gly	cga Arg	ggg Gly	gtt Val	gac Asp	ctg Leu	gta Val	gtc Val	gag Glu	gta Val	ggg Gly	ggg Gly	gcg Ala	720
225230235240																
ggg Gly	acc Thr	ttg Leu	gag Glu	cgc Arg	tca Ser	ctt Leu	cgt Arg	gcg Ala	gtc Val	aag Lys	gta Val	ggc Gly	ggt Gly	att Ile	gtc Val	768
245250255																
gcc Ala	acg Thr	att Ile	ggg Gly	cta Leu	gtg Val	gct Ala	ggc Gly	gtt Val	ggc Gly	ccg Pro	att Ile	gac Asp	cca Pro	ttg Leu	ccg Pro	816
260265270																
ctt Leu	atc Ile	tcc Ser	agg Arg	gct Ala	att Ile	cag Gln	ctc Leu	tcg Ser	ggc Gly	gtc Val	tat Tyr	gtc Val	ggt Gly	tcc Ser	cgg Arg	864
275280285																
gaa Glu	atg Met	ttt Phe	ctc Leu	tca Ser	atg Met	aac Asn	aaa Lys	gcc Ala	att Ile	gca Ala	tca Ser	gcc Ala	gaa Glu	atc Ile	aag Lys	912
290295300																
cca Pro	gtg Val	atc Ile	gat Asp	tgc Cys	tgc Cys	ttc Phe	ccc Pro	atc Ile	gac Asp	gag Glu	gtt Val	gga Gly	gat Asp	gct Ala	tat Tyr	960
305310315320																
gag Glu	tac Tyr	atg Met	cgt Arg	agc Ser	ggc Gly	aat Asn	cac His	ctt Leu	ggc Gly	aaa Lys	gta Val	gtt Val	atc Ile	acg Thr	atc Ile	1008
325330335																
taa1011																



<210> 20  
 <211> 336  
 <212> PRT  
 <213> not required under old rule

<400> 20

```

Met Lys Ala Tyr Glu Leu His Lys Ile Ser Glu Gln Val Glu Val Arg
 1           5           10           15
.
Leu Gln Pro Thr Arg Pro Arg Pro Gln Leu Asn His Gly Glu Val Leu
          20           25           30

Ile Arg Val His Ala Ala Ser Leu Asn Phe Arg Asp Leu Met Ile Leu
          35           40           45

Ala Gly Arg Tyr Pro Gly Gln Met Lys Pro Asp Val Ile Pro Leu Ser
          50           55           60

Asp Gly Ala Gly Glu Ile Val Glu Val Gly Pro Gly Val Ser Ser Glu
          65           70           75           80

Val Gln Gly Gln Arg Val Ala Ser Thr Phe Phe Pro Asn Trp Arg Ala
          85           90           95

Gly Lys Ile Thr Glu Pro Ala Ile Glu Val Ser Leu Gly Phe Gly Met
          100          105          110

Asp Gly Met Leu Ala Glu Tyr Val Ala Leu Pro Tyr Glu Ala Thr Ile
          115          120          125

Pro Ile Pro Glu His Leu Ser Tyr Glu Glu Ala Ala Thr Leu Pro Cys
          130          135          140

Ala Ala Leu Thr Ala Trp Asn Ala Leu Thr Glu Val Gly Arg Val Lys
          145          150          155          160

Ala Gly Asp Thr Val Leu Leu Leu Gly Thr Gly Gly Val Ser Met Phe
          165          170          175

Ala Leu Gln Phe Ala Lys Leu Leu Gly Ala Thr Val Ile His Thr Ser
          180          185          190

Ser Ser Glu Gln Lys Leu Glu Arg Val Lys Ala Met Gly Ala Asp His
          195          200          205

Leu Ile Asn Tyr Arg Asn Ser Pro Gly Trp Asp Arg Thr Val Leu Asp
          210          215          220

Leu Thr Ala Gly Arg Gly Val Asp Leu Val Val Glu Val Gly Gly Ala
          225          230          235          240

Gly Thr Leu Glu Arg Ser Leu Arg Ala Val Lys Val Gly Gly Ile Val
          245          250          255

```

Ala	Thr	Ile	Gly	Leu	Val	Ala	Gly	Val	Gly	Pro	Ile	Asp	Pro	Leu	Pro
			260					265					270		
Leu	Ile	Ser	Arg	Ala	Ile	Gln	Leu	Ser	Gly	Val	Tyr	Val	Gly	Ser	Arg
		275					280					285			
Glu	Met	Phe	Leu	Ser	Met	Asn	Lys	Ala	Ile	Ala	Ser	Ala	Glu	Ile	Lys
	290					295					300				
Pro	Val	Ile	Asp	Cys	Cys	Phe	Pro	Ile	Asp	Glu	Val	Gly	Asp	Ala	Tyr
305					310					315					320
Glu	Tyr	Met	Arg	Ser	Gly	Asn	His	Leu	Gly	Lys	Val	Val	Ile	Thr	Ile
				325					330					335	

<210> 21  
 <211> 1518  
 <212> DNA  
 <213> not required under old rule

<400> 21  
 tcaccgtcgt gatcgggatt ggaaattcgt gcgaggacag cggccacgta ccggcgcctt 60  
 gaagggctgg aaggttggag ttctgttaag gtctggtacc cagcagccat ggagagcggc 120  
 ccttagccgg aatggcagct tgatggttgc cacgggaacca gactggatgt cttgagtgtc 180  
 gagaattacc agatcgctgc gattttcatc gaggcgacca accacggtca gcaagtaccc 240  
 gtcaccttcg gcggcggctg gacttctagg gacgaaggcc ggctcctggg ccgccgaggg 300  
 ttcgccggag taccagaggt cgtagtcacc tcggtggttg tcccagatgc cgagtgagtt 360  
 gtacgcgaat atcttctcgg cctgctgatg cgcaagtggg ttgctgggat cgtccacccc 420  
 cataaagcca tagcggttgc attgcagggc gaacgaagaa tccatgattg gcatttccgc 480  
 aaagaaatcg ttagccggg ttcgcttgat ctgctcgtg ctgctatcga ggtcaatttc 540  
 ccaacgagtc aggcgtggta cggctttctc aggggcgaag ggttggtttt gtgagttggg 600  
 gaaggggaac ggcaggattt cactttccat aaggtcgata taaatcttgg ttccgacttc 660  
 ccaagcattc acaacatgaa ataccagag cgccggtgcc ttgagccagc gaatcagact 720  
 gccctggcgc ggcgcgagta cgccaatgta gctgccagc tccggctccc acatataaat 780  
 tggctgtttc gccttgaggc gggacaggct gttggtggcc ggcataattg ggaaaatgga 840  
 ccaatttcgg gtaatggcaa agtcgtgcat gaatgcgcca tagggctgct caaaccaagt 900  
 ttcatgtgtc accttgccgt gcttgctgac aatgtaatag gccatgtctg gagttgcttc 960  
 gcccttagct gccgaaccga agaacaacaa gtcacccggt tccgggtcat attttgatg 1020

ggcgggtgtgg gtttggtggtg taacttggcc gtcgtagtcg aagtgtccgc gagtttcaag 1080  
 tgtacgagga tccagttcgt acggtaggcc gtcttccttc accgccagca ccttgccgtg 1140  
 atggctaata atgcttgtat tggcaacggt gcggtctagt ccttttacac tgggtgcgtc 1200  
 ggtatagggg tttctgtaca tgccaaatag cgattttcgc gctagtcgtt cggccgtgaa 1260  
 tcgagcgggt ttaacccagc gactgatgaa gtcgacatga ccatcttcga agtggaaggc 1320  
 agaggccatt ccatctccat ctatgaaggt gtggaatttt tgtggggtaa cttgaggctc 1380  
 tggcgtatta cggtagaacg ttccatttat tgattttggg atttcgccgt caacctctag 1440  
 atcgaacaag tctgcctcta tacgggtggg gagaagtgtt cctactaatt gcgggtcgtt 1500  
 gcggttgaat ctgccat 1518

<210> 22  
 <211> 505  
 <212> PRT  
 <213> not required under old rule

<400> 22  
 Met Ala Arg Phe Asn Arg Asn Asp Pro Gln Leu Val Gly Thr Leu Leu  
 1 5 10 15  
 Pro Thr Arg Ile Glu Ala Asp Leu Phe Asp Leu Glu Val Asp Gly Glu  
 20 25 30  
 Ile Pro Lys Ser Ile Asn Gly Thr Phe Tyr Arg Asn Thr Pro Glu Pro  
 35 40 45  
 Gln Val Thr Pro Gln Lys Phe His Thr Phe Ile Asp Gly Asp Gly Met  
 50 55 60  
 Ala Ser Ala Phe His Phe Glu Asp Gly His Val Asp Phe Ile Ser Arg  
 65 70 75 80  
 Trp Val Lys Thr Ala Arg Phe Thr Ala Glu Arg Leu Ala Arg Lys Ser  
 85 90 95  
 Leu Phe Gly Met Tyr Arg Asn Pro Tyr Thr Asp Asp Thr Ser Val Lys  
 100 105 110  
 Gly Leu Asp Arg Thr Val Ala Asn Thr Ser Ile Ile Ser His His Gly  
 115 120 125  
 Lys Val Leu Ala Val Lys Glu Asp Gly Leu Pro Tyr Glu Leu Asp Pro  
 130 135 140  
 Arg Thr Leu Glu Thr Arg Gly His Phe Asp Tyr Asp Gly Gln Val Thr  
 145 150 155 160  
 Ser Gln Thr His Thr Ala His Pro Lys Tyr Asp Pro Glu Thr Gly Asp  
 165 170 175





tcc aat ccg gag gat ctt atc gcc cga cga gtt gat gct gag gta ggg	480
Ser Asn Pro Glu Asp Leu Ile Ala Arg Arg Val Asp Ala Glu Val Gly	
145 150 155 160	
tggt ggt agg gcg cta agc gca tgc gtt tct aat cta gat cca ttg cgc	528
Trp Gly Arg Ala Leu Ser Ala Ser Val Ser Asn Leu Asp Pro Leu Arg	
165 170 175	
atc gac gat tta ggt agc aat gta aat ggc att gca gag cat gtt gct	576
Ile Asp Asp Leu Gly Ser Asn Val Asn Gly Ile Ala Glu His Val Ala	
180 185 190	
atg tta att tca cta gca agt tct gcg gtt agt tct gaa gat ggg ggt	624
Met Leu Ile Ser Leu Ala Ser Ser Ala Val Ser Ser Glu Asp Gly Gly	
195 200 205	
gtg gct ctt cgg aaa atg agg gaa gtg aag aga gta ctc gag cag agt	672
Val Ala Leu Arg Lys Met Arg Glu Val Lys Arg Val Leu Glu Gln Ser	
210 215 220	
ttc gca gac gct aat ctc ggg ccg gaa agt gtt tca agt caa tta gga	720
Phe Ala Asp Ala Asn Leu Gly Pro Glu Ser Val Ser Ser Gln Leu Gly	
225 230 235 240	
att tgc aaa cgc tat ttg cat tat gtc ttt gct gcg tgc ggt acg acc	768
Ile Ser Lys Arg Tyr Leu His Tyr Val Phe Ala Ala Cys Gly Thr Thr	
245 250 255	
ttt ggt cgc gag ctg ttg gaa ata cgc ctg ggc aaa gct tat cga atg	816
Phe Gly Arg Glu Leu Leu Glu Ile Arg Leu Gly Lys Ala Tyr Arg Met	
260 265 270	
ctc tgt gcg gcg agt gac tgc ggt gct gtg ctg aag gtg gcc atg tcc	864
Leu Cys Ala Ala Ser Asp Ser Gly Ala Val Leu Lys Val Ala Met Ser	
275 280 285	
tca ggt ttt tgc gat tca agc cat ttc agc aag aaa ttt aag gaa aga	912
Ser Gly Phe Ser Asp Ser Ser His Phe Ser Lys Lys Phe Lys Glu Arg	
290 295 300	
tac ggt gtt tgc cct gtc tcc ttg gtg agg cag gct tga	951
Tyr Gly Val Ser Pro Val Ser Leu Val Arg Gln Ala	
305 310 315	

<210> 24

<211> 316

<212> PRT

<213> not required under old rule

<400> 24

Met Thr Thr Ile Arg Trp Arg Arg Met Ser Ile His Ser Glu Gly Ile
1 5 10 15

Thr Leu Ala Asp Ser Pro Leu His Trp Ala His Thr Leu Asn Gly Ser
20 25 30

Met	Arg	Thr	His	Phe	Glu	Val	Gln	Arg	Leu	Glu	Arg	Gly	Arg	Gly	Ala
		35					40					45			
Ser	Leu	Ala	Arg	Ser	Arg	Phe	Gly	Ala	Gly	Glu	Leu	Tyr	Ser	Ala	Ile
	50					55					60				
Ala	Pro	Ser	Gln	Val	Leu	Arg	His	Phe	Asn	Asp	Gln	Arg	Asn	Ala	Asp
	65				70					75					80
Glu	Ala	Glu	His	Ser	Tyr	Leu	Ile	Gln	Ile	Arg	Ser	Gly	Ala	Leu	Gly
				85					90					95	
Val	Ala	Ser	Gly	Gly	Arg	Lys	Val	Ile	Leu	Ala	Asn	Gly	Asp	Cys	Ser
			100					105					110		
Ile	Val	Asp	Ser	Arg	Gln	Asp	Phe	Thr	Leu	Ser	Ser	Asn	Ser	Ser	Thr
		115					120					125			
Gln	Gly	Val	Val	Ile	Arg	Phe	Pro	Val	Ser	Trp	Leu	Gly	Ala	Trp	Val
	130					135					140				
Ser	Asn	Pro	Glu	Asp	Leu	Ile	Ala	Arg	Arg	Val	Asp	Ala	Glu	Val	Gly
	145				150					155					160
Trp	Gly	Arg	Ala	Leu	Ser	Ala	Ser	Val	Ser	Asn	Leu	Asp	Pro	Leu	Arg
				165					170					175	
Ile	Asp	Asp	Leu	Gly	Ser	Asn	Val	Asn	Gly	Ile	Ala	Glu	His	Val	Ala
			180					185					190		
Met	Leu	Ile	Ser	Leu	Ala	Ser	Ser	Ala	Val	Ser	Ser	Glu	Asp	Gly	Gly
		195					200					205			
Val	Ala	Leu	Arg	Lys	Met	Arg	Glu	Val	Lys	Arg	Val	Leu	Glu	Gln	Ser
	210					215					220				
Phe	Ala	Asp	Ala	Asn	Leu	Gly	Pro	Glu	Ser	Val	Ser	Ser	Gln	Leu	Gly
	225				230					235					240
Ile	Ser	Lys	Arg	Tyr	Leu	His	Tyr	Val	Phe	Ala	Ala	Cys	Gly	Thr	Thr
				245					250					255	
Phe	Gly	Arg	Glu	Leu	Leu	Glu	Ile	Arg	Leu	Gly	Lys	Ala	Tyr	Arg	Met
			260					265					270		
Leu	Cys	Ala	Ala	Ser	Asp	Ser	Gly	Ala	Val	Leu	Lys	Val	Ala	Met	Ser
		275					280					285			
Ser	Gly	Phe	Ser	Asp	Ser	Ser	His	Phe	Ser	Lys	Lys	Phe	Lys	Glu	Arg
	290					295					300				
Tyr	Gly	Val	Ser	Pro	Val	Ser	Leu	Val	Arg	Gln	Ala				
	305				310					315					

<210> 25  
 <211> 735  
 <212> DNA  
 <213> not required under old rule

<220>  
 <221> CDS  
 <222> (1)..(732)  
 <223> product = "Enoyl-CoA-Hydratase" / gene = "ech"

<400> 25  
 atg agc cca act ctc aat cga gag atg gtc gag gtt ctg gag gtg ctg 48  
 Met Ser Pro Thr Leu Asn Arg Glu Met Val Glu Val Leu Glu Val Leu  
 1 5 10 15

gag cag gac gca gat gct cgc gtg ctt gtt ctg act ggt gca ggc gaa 96  
 Glu Gln Asp Ala Asp Ala Arg Val Leu Val Leu Thr Gly Ala Gly Glu  
 20 25 30

tcc tgg acc gcg ggc atg gac ctg aag gag tat ttc cgc gag acc gat 144  
 Ser Trp Thr Ala Gly Met Asp Leu Lys Glu Tyr Phe Arg Glu Thr Asp  
 35 40 45

gct ggc ccc gaa att ctg caa gag aag att cgt cgc gaa gcg tcg acc 192  
 Ala Gly Pro Glu Ile Leu Gln Glu Lys Ile Arg Arg Glu Ala Ser Thr  
 50 55 60

tgg cag tgg aag ctc ctg cgg atg tac acc aag ccg acc atc gcg atg 240  
 Trp Gln Trp Lys Leu Leu Arg Met Tyr Thr Lys Pro Thr Ile Ala Met  
 65 70 75 80

gtc aat ggc tgg tgc ttc ggc ggc ggc ttc agc ccg ctg gtg gcc tgt 288  
 Val Asn Gly Trp Cys Phe Gly Gly Gly Phe Ser Pro Leu Val Ala Cys  
 85 90 95

gat ctg gcc atc tgt gcc gac gag gcc acc ttt ggc ctg tcc gag atc 336  
 Asp Leu Ala Ile Cys Ala Asp Glu Ala Thr Phe Gly Leu Ser Glu Ile  
 100 105 110

aac tgg ggc atc ccg ccg ggc aac ctg gtg agt aag gct atg gcc gac 384  
 Asn Trp Gly Ile Pro Pro Gly Asn Leu Val Ser Lys Ala Met Ala Asp  
 115 120 125

acc gtg ggt cac cgc gag tcc ctt tac tac atc atg act ggc aag aca 432  
 Thr Val Gly His Arg Glu Ser Leu Tyr Tyr Ile Met Thr Gly Lys Thr  
 130 135 140

ttt ggc ggt cag cag gcc gcc aag atg ggg ctt gtg aac cag agt gtt 480  
 Phe Gly Gly Gln Gln Ala Ala Lys Met Gly Leu Val Asn Gln Ser Val  
 145 150 155 160

ccg ctg gcc gag ctg cgc agt gtc act gta gag ctg gct cag aac ctg 528  
 Pro Leu Ala Glu Leu Arg Ser Val Thr Val Glu Leu Ala Gln Asn Leu  
 165 170 175



003321 \* 98605460

```

ctg gac aag aac ccc gta gtg ctg cgt gcc gcc aaa ata ggc ttc aag 576
Leu Asp Lys Asn Pro Val Val Leu Arg Ala Ala Lys Ile Gly Phe Lys
      180              185              190

cgt tgc cgc gag ctg act tgg gag cag aac gag gac tac ctg tac gcc 624
Arg Cys Arg Glu Leu Thr Trp Glu Gln Asn Glu Asp Tyr Leu Tyr Ala
      195              200              205

aag ctc gac caa tcc cgt ttg ctc gat ccg gaa ggc ggt cgc gag cag 672
Lys Leu Asp Gln Ser Arg Leu Leu Asp Pro Glu Gly Gly Arg Glu Gln
      210              215              220

ggc atg aag cag ttc ctt gac gag aaa agc atc aag ccg ggc ttg cag 720
Gly Met Lys Gln Phe Leu Asp Glu Lys Ser Ile Lys Pro Gly Leu Gln
      225              230              235              240

acc tac aag cgc tga 735
Thr Tyr Lys Arg

```

```

<210> 26
<211> 244
<212> PRT
<213> not required under old rule

```

```

<400> 26
Met Ser Pro Thr Leu Asn Arg Glu Met Val Glu Val Leu Glu Val Leu
  1          5          10          15

Glu Gln Asp Ala Asp Ala Arg Val Leu Val Leu Thr Gly Ala Gly Glu
      20          25          30

Ser Trp Thr Ala Gly Met Asp Leu Lys Glu Tyr Phe Arg Glu Thr Asp
      35          40          45

Ala Gly Pro Glu Ile Leu Gln Glu Lys Ile Arg Arg Glu Ala Ser Thr
      50          55          60

Trp Gln Trp Lys Leu Leu Arg Met Tyr Thr Lys Pro Thr Ile Ala Met
      65          70          75          80

Val Asn Gly Trp Cys Phe Gly Gly Gly Phe Ser Pro Leu Val Ala Cys
      85          90          95

Asp Leu Ala Ile Cys Ala Asp Glu Ala Thr Phe Gly Leu Ser Glu Ile
      100         105         110

Asn Trp Gly Ile Pro Pro Gly Asn Leu Val Ser Lys Ala Met Ala Asp
      115         120         125

Thr Val Gly His Arg Glu Ser Leu Tyr Tyr Ile Met Thr Gly Lys Thr
      130         135         140

Phe Gly Gly Gln Gln Ala Ala Lys Met Gly Leu Val Asn Gln Ser Val
      145         150         155         160

```

Pro Leu Ala Glu Leu Arg Ser Val Thr Val Glu Leu Ala Gln Asn Leu  
165 170 175

Leu Asp Lys Asn Pro Val Val Leu Arg Ala Ala Lys Ile Gly Phe Lys  
180 185 190

Arg Cys Arg Glu Leu Thr Trp Glu Gln Asn Glu Asp Tyr Leu Tyr Ala  
195 200 205

Lys Leu Asp Gln Ser Arg Leu Leu Asp Pro Glu Gly Gly Arg Glu Gln  
210 215 220

Gly Met Lys Gln Phe Leu Asp Glu Lys Ser Ile Lys Pro Gly Leu Gln  
225 230 235 240

Thr Tyr Lys Arg

<210> 27  
<211> 1446  
<212> DNA  
<213> not required under old rule

<220>  
<221> CDS  
<222> (1)..(1443)  
<223> product = Vanillin-Dehydrogenase" / gene = "vdh"

<400> 27  
atg ttt cac gtg ccc ctg ctt att ggt ggt aag cct tgt tca gca tct 48  
Met Phe His Val Pro Leu Leu Ile Gly Gly Lys Pro Cys Ser Ala Ser  
1 5 10 15

gat gag cgc acc ttc gag cgt cgt agc ccg ctg acc gga gaa gtg gta 96  
Asp Glu Arg Thr Phe Glu Arg Arg Ser Pro Leu Thr Gly Glu Val Val  
20 25 30

tcg cgc gtc gct gct gcc agt ttg gaa gat gcg gac gcc gca gtg gcc 144  
Ser Arg Val Ala Ala Ala Ser Leu Glu Asp Ala Asp Ala Ala Val Ala  
35 40 45

gct gca cag gct gcg ttt cct gaa tgg gcg gcg ctt gct ccg agc gaa 192  
Ala Ala Gln Ala Ala Phe Pro Glu Trp Ala Ala Leu Ala Pro Ser Glu  
50 55 60

cgc cgt gcc cga ctg ctg cga gcg gcg gat ctt cta gag gac cgt tct 240  
Arg Arg Ala Arg Leu Leu Arg Ala Ala Asp Leu Leu Glu Asp Arg Ser  
65 70 75 80

tcc gag ttc acc gcc gca gcg agt gaa act ggc gca gcg gga aac tgg 288  
Ser Glu Phe Thr Ala Ala Ala Ser Glu Thr Gly Ala Ala Gly Asn Trp  
85 90 95

tat ggg ttt aac gtt tac ctg gcg gcg ggc atg ttg cgg gaa gcc gcg	336
Tyr Gly Phe Asn Val Tyr Leu Ala Ala Gly Met Leu Arg Glu Ala Ala	
100 105 110	
gcc atg acc aca cag att cag ggc gat gtc att ccg tcc aat gtg ccc	384
Ala Met Thr Thr Gln Ile Gln Gly Asp Val Ile Pro Ser Asn Val Pro	
115 120 125	
ggc agc ttt gcc atg gcg gtt cga cag cca tgt ggc gtg gtg ctc ggt	432
Gly Ser Phe Ala Met Ala Val Arg Gln Pro Cys Gly Val Val Leu Gly	
130 135 140	
att gcg cct tgg aat gct ccg gta atc ctt ggc gta cgg gct gtt gcg	480
Ile Ala Pro Trp Asn Ala Pro Val Ile Leu Gly Val Arg Ala Val Ala	
145 150 155 160	
atg ccg ttg gca tgc ggc aat acc gtg gtg ttg aaa agc tct gag ctg	528
Met Pro Leu Ala Cys Gly Asn Thr Val Val Leu Lys Ser Ser Glu Leu	
165 170 175	
agt ccc ttt acc cat cgc ctg att ggt cag gtg ttg cat gat gct ggt	576
Ser Pro Phe Thr His Arg Leu Ile Gly Gln Val Leu His Asp Ala Gly	
180 185 190	
ctg ggg gat ggc gtg gtg aat gtc atc agc aat gcc ccg caa gac gct	624
Leu Gly Asp Gly Val Val Asn Val Ile Ser Asn Ala Pro Gln Asp Ala	
195 200 205	
cct gcg gtg gtg gag cga ctg att gca aat cct gcg gta cgt cga gtg	672
Pro Ala Val Val Glu Arg Leu Ile Ala Asn Pro Ala Val Arg Arg Val	
210 215 220	
aac ttc acc ggt tcg acc cac gtt gga cgg atc att ggt gag ctg tct	720
Asn Phe Thr Gly Ser Thr His Val Gly Arg Ile Ile Gly Glu Leu Ser	
225 230 235 240	
gcg cgt cat ctg aag cct gct gtg ctg gaa tta ggt ggt aag gct ccg	768
Ala Arg His Leu Lys Pro Ala Val Leu Glu Leu Gly Gly Lys Ala Pro	
245 250 255	
ttc ttg gtc ttg gac gat gcc gac ctc gat gcg gcg gtc gaa gcg gcg	816
Phe Leu Val Leu Asp Asp Ala Asp Leu Asp Ala Ala Val Glu Ala Ala	
260 265 270	
gcc ttt ggt gcc tac ttc aat cag ggt caa atc tgc atg tcc act gag	864
Ala Phe Gly Ala Tyr Phe Asn Gln Gly Gln Ile Cys Met Ser Thr Glu	
275 280 285	
cgt ctg att gtg aca gca gtc gca gac gcc ttt gtt gaa aag ctg gcg	912
Arg Leu Ile Val Thr Ala Val Ala Asp Ala Phe Val Glu Lys Leu Ala	
290 295 300	
agg aag gtc gcc aca ctg cgt gct ggc gat cct aat gat ccg caa tcg	960
Arg Lys Val Ala Thr Leu Arg Ala Gly Asp Pro Asn Asp Pro Gln Ser	
305 310 315 320	

gtc ttg ggt tgc ttg att gat gcc aat gca ggt caa cgc atc cag gtt	1008
Val Leu Gly Ser Leu Ile Asp Ala Asn Ala Gly Gln Arg Ile Gln Val	
325 330 335	
ctg gtc gat gat gcg ctc gca aaa ggc gcg cgg cag gtc gtc ggt ggt	1056
Leu Val Asp Asp Ala Leu Ala Lys Gly Ala Arg Gln Val Val Gly Gly	
340 345 350	
ggc tta gat ggc agc atc atg cag ccg atg ctg ctt gat cag gtc act	1104
Gly Leu Asp Gly Ser Ile Met Gln Pro Met Leu Leu Asp Gln Val Thr	
355 360 365	
gaa gag atg cgg ctc tac cgt gag gag tcc ttt ggc cct gtt gcc gtt	1152
Glu Glu Met Arg Leu Tyr Arg Glu Glu Ser Phe Gly Pro Val Ala Val	
370 375 380	
gtc ttg cgc ggc gat ggt gat gaa gaa ctg ctg cgt ctt gcc aac gat	1200
Val Leu Arg Gly Asp Gly Asp Glu Glu Leu Leu Arg Leu Ala Asn Asp	
385 390 395 400	
tgc gag ttt ggt ctt tgc gcc gcc att ttc agc cgt gac gtc tgc cgc	1248
Ser Glu Phe Gly Leu Ser Ala Ala Ile Phe Ser Arg Asp Val Ser Arg	
405 410 415	
gca atg gaa ttg gcc cag cgc gtc gat tgc ggc att tgc cat atc aat	1296
Ala Met Glu Leu Ala Gln Arg Val Asp Ser Gly Ile Cys His Ile Asn	
420 425 430	
gga ccg act gtg cat gac gag gct cag atg cca ttc ggt ggg gtg aag	1344
Gly Pro Thr Val His Asp Glu Ala Gln Met Pro Phe Gly Gly Val Lys	
435 440 445	
tcc agc ggc tac ggc agc ttc ggc agt cga gca tgc att gag cac ttt	1392
Ser Ser Gly Tyr Gly Ser Phe Gly Ser Arg Ala Ser Ile Glu His Phe	
450 455 460	
acc cag ctg cgc tgg ctg acc att cag aat ggc ccg cgg cac tat cca	1440
Thr Gln Leu Arg Trp Leu Thr Ile Gln Asn Gly Pro Arg His Tyr Pro	
465 470 475 480	
atc taa	1446
Ile	

<210> 28

<211> 481

<212> PRT

<213> not required under old rule

<400> 28

Met	Phe	His	Val	Pro	Leu	Leu	Ile	Gly	Gly	Lys	Pro	Cys	Ser	Ala	Ser
1				5				10						15	

Asp	Glu	Arg	Thr	Phe	Glu	Arg	Arg	Ser	Pro	Leu	Thr	Gly	Glu	Val	Val
	20							25					30		

Ser	Arg	Val	Ala	Ala	Ala	Ser	Leu	Glu	Asp	Ala	Asp	Ala	Ala	Val	Ala
		35					40				45				
Ala	Ala	Gln	Ala	Ala	Phe	Pro	Glu	Trp	Ala	Ala	Leu	Ala	Pro	Ser	Glu
50						55				60					
Arg	Arg	Ala	Arg	Leu	Leu	Arg	Ala	Ala	Asp	Leu	Leu	Glu	Asp	Arg	Ser
65					70				75				80		
Ser	Glu	Phe	Thr	Ala	Ala	Ala	Ser	Glu	Thr	Gly	Ala	Ala	Gly	Asn	Trp
				85				90						95	
Tyr	Gly	Phe	Asn	Val	Tyr	Leu	Ala	Ala	Gly	Met	Leu	Arg	Glu	Ala	Ala
		100						105				110			
Ala	Met	Thr	Thr	Gln	Ile	Gln	Gly	Asp	Val	Ile	Pro	Ser	Asn	Val	Pro
		115				120						125			
Gly	Ser	Phe	Ala	Met	Ala	Val	Arg	Gln	Pro	Cys	Gly	Val	Val	Leu	Gly
130						135				140					
Ile	Ala	Pro	Trp	Asn	Ala	Pro	Val	Ile	Leu	Gly	Val	Arg	Ala	Val	Ala
145					150				155				160		
Met	Pro	Leu	Ala	Cys	Gly	Asn	Thr	Val	Val	Leu	Lys	Ser	Ser	Glu	Leu
				165				170						175	
Ser	Pro	Phe	Thr	His	Arg	Leu	Ile	Gly	Gln	Val	Leu	His	Asp	Ala	Gly
		180						185				190			
Leu	Gly	Asp	Gly	Val	Val	Asn	Val	Ile	Ser	Asn	Ala	Pro	Gln	Asp	Ala
		195				200						205			
Pro	Ala	Val	Val	Glu	Arg	Leu	Ile	Ala	Asn	Pro	Ala	Val	Arg	Arg	Val
210						215				220					
Asn	Phe	Thr	Gly	Ser	Thr	His	Val	Gly	Arg	Ile	Ile	Gly	Glu	Leu	Ser
225					230				235				240		
Ala	Arg	His	Leu	Lys	Pro	Ala	Val	Leu	Glu	Leu	Gly	Gly	Lys	Ala	Pro
				245				250						255	
Phe	Leu	Val	Leu	Asp	Asp	Ala	Asp	Leu	Asp	Ala	Ala	Val	Glu	Ala	Ala
		260						265				270			
Ala	Phe	Gly	Ala	Tyr	Phe	Asn	Gln	Gly	Gln	Ile	Cys	Met	Ser	Thr	Glu
		275				280						285			
Arg	Leu	Ile	Val	Thr	Ala	Val	Ala	Asp	Ala	Phe	Val	Glu	Lys	Leu	Ala
290						295				300					
Arg	Lys	Val	Ala	Thr	Leu	Arg	Ala	Gly	Asp	Pro	Asn	Asp	Pro	Gln	Ser
305					310				315				320		
Val	Leu	Gly	Ser	Leu	Ile	Asp	Ala	Asn	Ala	Gly	Gln	Arg	Ile	Gln	Val
				325				330						335	

Leu Val Asp Asp Ala Leu Ala Lys Gly Ala Arg Gln Val Val Gly Gly  
 340 345 350

Gly Leu Asp Gly Ser Ile Met Gln Pro Met Leu Leu Asp Gln Val Thr  
 355 360 365

Glu Glu Met Arg Leu Tyr Arg Glu Glu Ser Phe Gly Pro Val Ala Val  
 370 375 380

Val Leu Arg Gly Asp Gly Asp Glu Glu Leu Leu Arg Leu Ala Asn Asp  
 385 390 395 400

Ser Glu Phe Gly Leu Ser Ala Ala Ile Phe Ser Arg Asp Val Ser Arg  
 405 410 415

Ala Met Glu Leu Ala Gln Arg Val Asp Ser Gly Ile Cys His Ile Asn  
 420 425 430

Gly Pro Thr Val His Asp Glu Ala Gln Met Pro Phe Gly Gly Val Lys  
 435 440 445

Ser Ser Gly Tyr Gly Ser Phe Gly Ser Arg Ala Ser Ile Glu His Phe  
 450 455 460

Thr Gln Leu Arg Trp Leu Thr Ile Gln Asn Gly Pro Arg His Tyr Pro  
 465 470 475 480

Ile

<210> 29  
 <211> 1770  
 <212> DNA  
 <213> not required under old rule

<220>  
 <221> CDS  
 <222> (1)..(1767)  
 <223> product = "Ferulasaeure-CoA-Synthetase" / gene =  
 "fcs"

<400> 29  
 atg cgt tct ctc gag gcg ctt ctt ccc ttc ccg ggt cga att ctt gag 48  
 Met Arg Ser Leu Glu Ala Leu Leu Pro Phe Pro Gly Arg Ile Leu Glu  
 1 5 10 15

cgt ctc gag cat tgg gct aag acc cgt cca gaa caa acc tgc gtt gct 96  
 Arg Leu Glu His Trp Ala Lys Thr Arg Pro Glu Gln Thr Cys Val Ala  
 20 25 30

gcc agg gcg gca aat ggg gaa tgg cgt cgt atc agc tac gcg gaa atg 144  
 Ala Arg Ala Ala Asn Gly Glu Trp Arg Arg Ile Ser Tyr Ala Glu Met  
 35 40 45

ttc	cac	aac	gtc	cgc	gcc	atc	gca	cag	agc	ttg	ctt	cct	tac	gga	cta	192
Phe	His	Asn	Val	Arg	Ala	Ile	Ala	Gln	Ser	Leu	Leu	Pro	Tyr	Gly	Leu	
50						55			60							
tcg	gca	gag	cgt	ccg	ctg	ctt	atc	gtc	tct	gga	aat	gac	ctg	gaa	cat	240
Ser	Ala	Glu	Arg	Pro	Leu	Leu	Ile	Val	Ser	Gly	Asn	Asp	Leu	Glu	His	
65			70						75			80				
ctt	cag	ctg	gca	ttt	ggg	gct	atg	tat	gcg	ggc	att	ccc	tat	tgc	ccg	288
Leu	Gln	Leu	Ala	Phe	Gly	Ala	Met	Tyr	Ala	Gly	Ile	Pro	Tyr	Cys	Pro	
			85						90			95				
gtg	tct	cct	gct	tat	tca	ctg	ctg	tcg	caa	gat	ttg	gcg	aag	ctg	cgt	336
Val	Ser	Pro	Ala	Tyr	Ser	Leu	Leu	Ser	Gln	Asp	Leu	Ala	Lys	Leu	Arg	
			100			105						110				
cac	atc	gta	ggg	ctt	ctg	caa	ccg	gga	ctg	gtc	ttt	gct	gcc	gat	gca	384
His	Ile	Val	Gly	Leu	Leu	Gln	Pro	Gly	Leu	Val	Phe	Ala	Ala	Asp	Ala	
115						120						125				
gca	cct	ttc	cag	cgc	gca	att	gag	acc	att	ctg	ccg	gac	gac	gtg	ccc	432
Ala	Pro	Phe	Gln	Arg	Ala	Ile	Glu	Thr	Ile	Leu	Pro	Asp	Asp	Val	Pro	
130						135			140							
gca	atc	ttc	act	cga	ggc	gaa	ttg	gcc	ggg	cgg	cgc	acg	gtg	agt	ttt	480
Ala	Ile	Phe	Thr	Arg	Gly	Glu	Leu	Ala	Gly	Arg	Arg	Thr	Val	Ser	Phe	
145			150						155			160				
gac	agc	ctg	ctg	gag	cag	cct	ggg	ggg	att	gag	gca	gat	aat	gcc	ttt	528
Asp	Ser	Leu	Leu	Glu	Gln	Pro	Gly	Gly	Ile	Glu	Ala	Asp	Asn	Ala	Phe	
			165						170			175				
gcg	gca	act	ggc	ccc	gat	acg	att	gcc	aag	ttc	ttg	ttc	act	tct	ggc	576
Ala	Ala	Thr	Gly	Pro	Asp	Thr	Ile	Ala	Lys	Phe	Leu	Phe	Thr	Ser	Gly	
180						185						190				
tct	acc	aaa	ctg	cct	aag	gcg	gtg	ccg	act	act	cag	cga	atg	ctc	tgc	624
Ser	Thr	Lys	Leu	Pro	Lys	Ala	Val	Pro	Thr	Thr	Gln	Arg	Met	Leu	Cys	
195						200			205							
gcc	aat	cag	cag	atg	ctt	ctg	caa	act	ttc	ccg	gtt	ttt	ggg	gaa	gag	672
Ala	Asn	Gln	Gln	Met	Leu	Leu	Gln	Thr	Phe	Pro	Val	Phe	Gly	Glu	Glu	
210						215			220							
ccg	ccg	gtg	ctg	gtg	gac	tgg	ttg	ccg	tgg	aac	cac	acc	ttc	ggc	ggc	720
Pro	Pro	Val	Leu	Val	Asp	Trp	Leu	Pro	Trp	Asn	His	Thr	Phe	Gly	Gly	
225			230						235			240				
agc	cac	aac	atc	ggc	atc	gtg	ttg	tac	aac	ggc	ggc	acg	tac	tac	ctt	768
Ser	His	Asn	Ile	Gly	Ile	Val	Leu	Tyr	Asn	Gly	Gly	Thr	Tyr	Tyr	Leu	
			245						250			255				
gac	gac	ggg	aaa	cca	acc	gcc	caa	ggg	ttc	gcc	gag	acg	ctt	cgc	aac	816
Asp	Asp	Gly	Lys	Pro	Thr	Ala	Gln	Gly	Phe	Ala	Glu	Thr	Leu	Arg	Asn	
260						265						270				

ttg agc gaa atc tct ccc act gcg tac ctc act gtg ccg aaa ggc tgg	864
Leu Ser Glu Ile Ser Pro Thr Ala Tyr Leu Thr Val Pro Lys Gly Trp	
275 280 285	
gag gaa tta gtg ggt gcc ctt gag cga gac agt acc ctg cgc gaa cgc	912
Glu Glu Leu Val Gly Ala Leu Glu Arg Asp Ser Thr Leu Arg Glu Arg	
290 295 300	
ttc ttc gct cgc atg aag ctg ttc ttc ttc gcg gcg gct ggg ttg tcg	960
Phe Phe Ala Arg Met Lys Leu Phe Phe Phe Ala Ala Ala Gly Leu Ser	
305 310 315 320	
caa ggg atc tgg gat cgt ttg gac cgg gtc gct gaa cag cac tgt ggt	1008
Gln Gly Ile Trp Asp Arg Leu Asp Arg Val Ala Glu Gln His Cys Gly	
325 330 335	
gag cgc att cgc atg atg gcg ggt ctg ggc atg acg gag act gct cct	1056
Glu Arg Ile Arg Met Met Ala Gly Leu Gly Met Thr Glu Thr Ala Pro	
340 345 350	
tcc tgc act ttt acc acc gga ccg ctg tcg atg gct ggt tac att ggg	1104
Ser Cys Thr Phe Thr Thr Gly Pro Leu Ser Met Ala Gly Tyr Ile Gly	
355 360 365	
ctg cca gcg cct ggc tgc gag gtc aag ctc gtt ccg gtc gat ggg aaa	1152
Leu Pro Ala Pro Gly Cys Glu Val Lys Leu Val Pro Val Asp Gly Lys	
370 375 380	
ttg gaa ggg cgt ttc cat ggt ccg cac gtc atg agc ggc tac tgg cgt	1200
Leu Glu Gly Arg Phe His Gly Pro His Val Met Ser Gly Tyr Trp Arg	
385 390 395 400	
gct cct gaa caa aat gcc caa gcg ttc gac gag gaa ggc tat tac tgc	1248
Ala Pro Glu Gln Asn Ala Gln Ala Phe Asp Glu Glu Gly Tyr Tyr Cys	
405 410 415	
tcc ggt gat gcc atc aaa ttg gca gat cct gcc gat cct cag aaa ggt	1296
Ser Gly Asp Ala Ile Lys Leu Ala Asp Pro Ala Asp Pro Gln Lys Gly	
420 425 430	
ctg atg ttt gac ggt cga att gct gaa gac ttc aag ctg tcc tca ggg	1344
Leu Met Phe Asp Gly Arg Ile Ala Glu Asp Phe Lys Leu Ser Ser Gly	
435 440 445	
gta ttt gtc agc gtt ggg cca ttg cgc acg cgg gcg gtt ctg gaa ggc	1392
Val Phe Val Ser Val Gly Pro Leu Arg Thr Arg Ala Val Leu Glu Gly	
450 455 460	
ggc tct tac gtc ctg gac gta gtg gtt gct gct cct gat cgt gaa tgc	1440
Gly Ser Tyr Val Leu Asp Val Val Val Ala Ala Pro Asp Arg Glu Cys	
465 470 475 480	
ctt gga ttg ctc gtg ttt ccg cgt ctt ctc gac tgc cgt gcc ttg tcg	1488
Leu Gly Leu Leu Val Phe Pro Arg Leu Leu Asp Cys Arg Ala Leu Ser	
485 490 495	





Ala	Ile	Phe	Thr	Arg	Gly	Glu	Leu	Ala	Gly	Arg	Arg	Thr	Val	Ser	Phe	
145					150					155					160	
Asp	Ser	Leu	Leu	Glu	Gln	Pro	Gly	Gly	Ile	Glu	Ala	Asp	Asn	Ala	Phe	
				165					170					175		
Ala	Ala	Thr	Gly	Pro	Asp	Thr	Ile	Ala	Lys	Phe	Leu	Phe	Thr	Ser	Gly	
			180					185						190		
Ser	Thr	Lys	Leu	Pro	Lys	Ala	Val	Pro	Thr	Thr	Gln	Arg	Met	Leu	Cys	
		195					200					205				
Ala	Asn	Gln	Gln	Met	Leu	Leu	Gln	Thr	Phe	Pro	Val	Phe	Gly	Glu	Glu	
	210						215				220					
Pro	Pro	Val	Leu	Val	Asp	Trp	Leu	Pro	Trp	Asn	His	Thr	Phe	Gly	Gly	
225					230					235					240	
Ser	His	Asn	Ile	Gly	Ile	Val	Leu	Tyr	Asn	Gly	Gly	Thr	Tyr	Tyr	Leu	
				245					250					255		
Asp	Asp	Gly	Lys	Pro	Thr	Ala	Gln	Gly	Phe	Ala	Glu	Thr	Leu	Arg	Asn	
			260					265					270			
Leu	Ser	Glu	Ile	Ser	Pro	Thr	Ala	Tyr	Leu	Thr	Val	Pro	Lys	Gly	Trp	
		275					280					285				
Glu	Glu	Leu	Val	Gly	Ala	Leu	Glu	Arg	Asp	Ser	Thr	Leu	Arg	Glu	Arg	
	290					295					300					
Phe	Phe	Ala	Arg	Met	Lys	Leu	Phe	Phe	Phe	Ala	Ala	Ala	Gly	Leu	Ser	
305					310					315					320	
Gln	Gly	Ile	Trp	Asp	Arg	Leu	Asp	Arg	Val	Ala	Glu	Gln	His	Cys	Gly	
				325					330					335		
Glu	Arg	Ile	Arg	Met	Met	Ala	Gly	Leu	Gly	Met	Thr	Glu	Thr	Ala	Pro	
			340					345					350			
Ser	Cys	Thr	Phe	Thr	Thr	Gly	Pro	Leu	Ser	Met	Ala	Gly	Tyr	Ile	Gly	
		355					360					365				
Leu	Pro	Ala	Pro	Gly	Cys	Glu	Val	Lys	Leu	Val	Pro	Val	Asp	Gly	Lys	
	370					375					380					
Leu	Glu	Gly	Arg	Phe	His	Gly	Pro	His	Val	Met	Ser	Gly	Tyr	Trp	Arg	
385					390					395					400	
Ala	Pro	Glu	Gln	Asn	Ala	Gln	Ala	Phe	Asp	Glu	Glu	Gly	Tyr	Tyr	Cys	
				405					410					415		
Ser	Gly	Asp	Ala	Ile	Lys	Leu	Ala	Asp	Pro	Ala	Asp	Pro	Gln	Lys	Gly	
			420					425					430			
Leu	Met	Phe	Asp	Gly	Arg	Ile	Ala	Glu	Asp	Phe	Lys	Leu	Ser	Ser	Gly	
	435						440					445				

Val Phe Val Ser Val Gly Pro Leu Arg Thr Arg Ala Val Leu Glu Gly  
 450 455 460

Gly Ser Tyr Val Leu Asp Val Val Val Ala Ala Pro Asp Arg Glu Cys  
 465 470 475 480

Leu Gly Leu Leu Val Phe Pro Arg Leu Leu Asp Cys Arg Ala Leu Ser  
 485 490 495

Gly Leu Gly Lys Glu Ala Ser Asp Ala Glu Val Leu Ala Ser Glu Pro  
 500 505 510

Val Arg Ala Trp Phe Ala Asp Trp Leu Lys Arg Leu Asn Arg Glu Ala  
 515 520 525

Thr Gly Asn Ala Ser Arg Ile Met Trp Val Gly Leu Leu Asp Thr Pro  
 530 535 540

Pro Ser Ile Asp Lys Gly Glu Val Thr Asp Lys Gly Ser Ile Asn Gln  
 545 550 555 560

Arg Ala Val Leu Gln Trp Arg Ser Ala Lys Val Asp Ala Leu Tyr Arg  
 565 570 575

Gly Glu Asp Gln Ser Met Leu Arg Asp Glu Ala Thr Leu  
 580 585

<210> 31  
 <211> 1296  
 <212> DNA  
 <213> not required under old rule

<220>  
 <221> CDS  
 <222> (1)..(1293)  
 <223> product = "beta-Ketothiolase" / gene = "aat"

<400> 31  
 atg agt tgg tca ggg ggg gct tac tcg gcg ttt tcc gac act gcg ttg 48  
 Met Ser Trp Ser Gly Gly Ala Tyr Ser Ala Phe Ser Asp Thr Ala Leu  
 1 5 10 15

gtt gcg gca gtg cgc acc ccc tgg att gat tgc ggg ggt gcc ctg tcg 96  
 Val Ala Ala Val Arg Thr Pro Trp Ile Asp Cys Gly Gly Ala Leu Ser  
 20 25 30

ctg gtg tcg cct atc gac tta ggg gta aag gtc gct cgc gaa gtt ctg 144  
 Leu Val Ser Pro Ile Asp Leu Gly Val Lys Val Ala Arg Glu Val Leu  
 35 40 45

atg cgt gcg tcg ctt gaa cca caa atg gtc gat agc gta ctc gca ggc 192  
 Met Arg Ala Ser Leu Glu Pro Gln Met Val Asp Ser Val Leu Ala Gly  
 50 55 60

tct Ser 65	atg Met	gct Ala	caa Gln	gca Ala	agc Ser	ttt Phe	gat Asp	gct Ala	tac Tyr	ctg Leu	ctc Leu	ccg Pro	cgg Arg	cac His	att Ile	240
					70								80			
ggc Gly	ttg Leu	tac Tyr	agc Ser	ggg Gly	gtt Val	ccc Pro	aag Lys	tcg Ser	ggt Val	ccg Pro	gcc Ala	ttg Leu	ggg Gly	gtg Val	cag Gln	288
					85								95			
cgc Arg	att Ile	tgc Cys	ggc Gly	aca Thr	ggc Gly	ttc Phe	gaa Glu	ctg Leu	ctt Leu	cgg Arg	cag Gln	gcc Ala	ggc Gly	gag Glu	cag Gln	336
					100								110			
att Ile	tcc Ser	caa Gln	ggc Gly	gct Ala	gat Asp	cac His	gtg Val	ctg Leu	tgt Cys	gtc Val	gcg Ala	gca Ala	gag Glu	tcc Ser	atg Met	384
					115								125			
tcg Ser	cgt Arg	aac Asn	ccc Pro	atc Ile	gcg Ala	tcg Ser	tat Tyr	aca Thr	cac His	cgg Arg	ggc Gly	ggg Gly	ttc Phe	cgc Arg	ctc Leu	432
					130								140			
ggg Gly 145	gcg Ala	ccc Pro	gtt Val	gag Glu	ttc Phe	aag Lys	gat Asp	ttt Phe	ttg Leu	tgg Trp	gag Glu	gca Ala	ttg Leu	ttt Phe	gat Asp 160	480
					150								155			
cct Pro	gct Ala	cca Pro	gga Gly	ctc Leu	gac Asp	atg Met	atc Ile	gct Ala	acc Thr	gca Ala	gaa Glu	aac Asn	ctg Leu	gcg Ala	cgc Arg	528
					165								170			
ctg Leu	tac Tyr	gga Gly	atc Ile	acc Thr	agg Arg	gga Gly	gaa Glu	gct Ala	aat Asn	tcc Ser	tac Tyr	gcg Ala	gta Val	agc Ser	agc Ser	576
					180								185			
ttc Phe	gag Glu	cgc Arg	gca Ala	ttg Leu	agg Arg	gcg Ala	caa Gln	gag Glu	gag Glu	aaa Lys	tgg Trp	att Ile	gac Asp	caa Gln	gag Glu	624
					195								200			
atc Ile	gtg Val	gct Ala	gtt Val	acg Thr	gat Asp	gaa Glu	cag Gln	ttc Phe	gat Asp	tta Leu	gag Glu	ggc Gly	tac Tyr	aac Asn	agt Ser	672
					210								215			
cga Arg 225	gca Ala	att Ile	gaa Glu	ctg Leu	cct Pro	cgg Arg	aag Lys	gca Ala	aaa Lys	ttg Leu	ttg Leu	atc Ile	gtg Val	aca Thr	gtc Val 240	720
					225								230			
atc Ile	cgc Arg	ggc Gly	cta Leu	gca Ala	gtc Val	ttt Phe	gaa Glu	gcc Ala	ctt Leu	tcc Ser	cga Arg	ttg Leu	aag Lys	cct Pro	gtt Val	768
					245								250			
cat His	tct Ser	ggc Gly	ggg Gly	gtg Val	cag Gln	act Thr	gcg Ala	ggc Gly	aac Asn	agc Ser	tgt Cys	gcc Ala	gta Val	gtg Val	gac Asp	816
					260								265			
ggc Gly	gcc Ala	gcg Ala	gcg Ala	gct Ala	ttg Leu	gtg Val	gct Ala	cga Arg	gag Glu	tcg Ser	tct Ser	gcg Ala	aca Thr	cag Gln	ccg Pro	864
					275								280			

gtc	ttg	gct	agg	ata	ctg	gct	acc	tcc	gta	gtc	ggg	atc	gag	ccc	gag	912
Val	Leu	Ala	Arg	Ile	Leu	Ala	Thr	Ser	Val	Val	Gly	Ile	Glu	Pro	Glu	
290 295 300																
cat	atg	ggg	ctc	ggc	cct	gcg	ccc	gcg	att	cgc	ctg	ctg	ctt	gcg	cgt	960
His	Met	Gly	Leu	Gly	Pro	Ala	Pro	Ala	Ile	Arg	Leu	Leu	Leu	Ala	Arg	
305 310 315 320																
agt	gat	ctt	agt	ttg	agg	gat	atc	gac	ctc	ttt	gag	ata	aac	gag	gcg	1008
Ser	Asp	Leu	Ser	Leu	Arg	Asp	Ile	Asp	Leu	Phe	Glu	Ile	Asn	Glu	Ala	
325 330 335																
cag	gcc	gcc	caa	gtt	cta	gcg	gta	cag	cat	gaa	ttg	ggg	att	gag	cac	1056
Gln	Ala	Ala	Gln	Val	Leu	Ala	Val	Gln	His	Glu	Leu	Gly	Ile	Glu	His	
340 345 350																
tca	aaa	ctt	aat	att	tgg	ggc	ggg	gcc	att	gca	ctt	gga	cac	ccg	ctt	1104
Ser	Lys	Leu	Asn	Ile	Trp	Gly	Gly	Ala	Ile	Ala	Leu	Gly	His	Pro	Leu	
355 360 365																
gcc	gcg	acc	gga	ttg	cgt	ctc	tgc	atg	acc	ctc	gct	cac	caa	ttg	caa	1152
Ala	Ala	Thr	Gly	Leu	Arg	Leu	Cys	Met	Thr	Leu	Ala	His	Gln	Leu	Gln	
370 375 380																
gct	aat	aac	ttt	cga	tat	gga	att	gcc	tcg	gca	tgc	att	ggg	ggg	gga	1200
Ala	Asn	Asn	Phe	Arg	Tyr	Gly	Ile	Ala	Ser	Ala	Cys	Ile	Gly	Gly	Gly	
385 390 395 400																
cag	ggg	atg	gcg	gtt	ctt	tta	gag	aat	ccc	cac	ttc	ggg	tcg	tcc	tct	1248
Gln	Gly	Met	Ala	Val	Leu	Leu	Glu	Asn	Pro	His	Phe	Gly	Ser	Ser	Ser	
405 410 415																
gca	cga	agt	tcg	atg	att	aac	aga	gtt	gac	cac	tat	cca	ctg	agc	taa	1296
Ala	Arg	Ser	Ser	Met	Ile	Asn	Arg	Val	Asp	His	Tyr	Pro	Leu	Ser		
420 425 430																
<210> 32																
<211> 431																
<212> PRT																
<213> not required under old rule																

<400> 32

Val Ala Ala Val Arg Thr Pro Trp Ile Asp Cys Gly Gly Ala Leu Ser  
20 25 30

Met Arg Ala Ser Leu Glu Pro Gln Met Val Asp Ser Val Leu Ala Gly  
50 55 60



Ala Asn Asn Phe Arg Tyr Gly Ile Ala Ser Ala Cys Ile Gly Gly Gly  
 385 390 395 400

Gln Gly Met Ala Val Leu Leu Glu Asn Pro His Phe Gly Ser Ser Ser  
 405 410 415

Ala Arg Ser Ser Met Ile Asn Arg Val Asp His Tyr Pro Leu Ser  
 420 425 430

<210> 33  
 <211> 1596  
 <212> DNA  
 <213> not required under old rule

<220>  
 <221> CDS  
 <222> (1)..(1593)  
 <223> product = "Chemotaxis-Protein" / gene = "mac"

<400> 33  
 atg att agt ttc gct cgt atg gca gaa agt tta gga gtc cag gct aaa 48  
 Met Ile Ser Phe Ala Arg Met Ala Glu Ser Leu Gly Val Gln Ala Lys  
 1 5 10 15

ctt gcc ctt gcc ttc gca ctc gta tta tgt gtc ggg ctg att gtt acc 96  
 Leu Ala Leu Ala Phe Ala Leu Val Leu Cys Val Gly Leu Ile Val Thr  
 20 25 30

ggc acg ggt ttc tac agt gta cat acc ttg tca ggg ttg gtg gaa aag 144  
 Gly Thr Gly Phe Tyr Ser Val His Thr Leu Ser Gly Leu Val Glu Lys  
 35 40 45

agc gcg ata gct ggt gag ttg cgg gcg aaa att cag gaa ctg aag gtt 192  
 Ser Ala Ile Ala Gly Glu Leu Arg Ala Lys Ile Gln Glu Leu Lys Val  
 50 55 60

ctg gag cag cgc gcc tta ttc atc gcc gat gaa ggg tcg ctg aag cag 240  
 Leu Glu Gln Arg Ala Leu Phe Ile Ala Asp Glu Gly Ser Leu Lys Gln  
 65 70 75 80

cgc tcg atc ctc cta agt cag gtg ata gct gaa gtt aat gat gct ata 288  
 Arg Ser Ile Leu Leu Ser Gln Val Ile Ala Glu Val Asn Asp Ala Ile  
 85 90 95

gat att ttt gac ttt cag cgc gga cga tct gag tta ctt aaa ttc gct 336  
 Asp Ile Phe Asp Phe Gln Arg Gly Arg Ser Glu Leu Leu Lys Phe Ala  
 100 105 110

gct tct tcg cgc gaa gca agt tac tcc att gag gtc ggt agt aac gct 384  
 Ala Ser Ser Arg Glu Ala Ser Tyr Ser Ile Glu Val Gly Ser Asn Ala  
 115 120 125

gcg Ala	gcc Ala	gat Asp	aag Lys	ttg Leu	cag Gln	tcg Ser	ggc Gly	gaa Glu	cca Pro	agt Ser	gac Asp	gca Ala	ttg Leu	atg Met	gtt Val	432
130			135			140										
gcc Ala	gat Asp	aaa Lys	aag Lys	ctg Leu	aat Asn	gtt Val	gag Glu	tat Tyr	gag Glu	caa Gln	ttg Leu	agt Ser	tct Ser	gct Ala	gtg Val	480
145			150			155			160							
aat Asn	gca Ala	ctg Leu	atg Met	ggg Gly	cat His	tta Leu	att Ile	gag Glu	gat Asp	cag Gln	aat Asn	gaa Glu	aaa Lys	gtt Val	cca Pro	528
165				170				175								
cta Leu	atc Ile	tac Tyr	tat Tyr	atg Met	ctt Leu	ggc Gly	ggc Gly	gta Val	act Thr	ttg Leu	ttt Phe	acg Thr	atg Met	ctc Leu	atg Met	576
180				185				190								
agt Ser	gct Ala	tat Tyr	tcg Ser	gtc Val	tgg Trp	ttc Phe	att Ile	tcg Ser	cgt Arg	cag Gln	tta Leu	gtt Val	ccg Pro	cca Pro	tta Leu	624
195			200			205										
aag Lys	tcg Ser	acg Thr	gtg Val	cag Gln	ctt Leu	gcc Ala	gag Glu	cgg Arg	att Ile	gca Ala	tca Ser	ggc Gly	gac Asp	ttg Leu	gct Ala	672
210			215			220										
gat Asp	gtc Val	ggg Gly	gac Asp	agc Ser	agg Arg	cgc Arg	aag Lys	gat Asp	gaa Glu	atc Ile	ggt Gly	cag Gln	ttg Leu	caa Gln	agt Ser	720
225			230			235			240							
gca Ala	act Thr	agg Arg	cgg Arg	atg Met	gcg Ala	att Ile	gga Gly	ctg Leu	cgt Arg	aat Asn	ctg Leu	gtc Val	ggg Gly	gat Asp	att Ile	768
245				250				255								
ggt Gly	caa Gln	agt Ser	cgt Arg	gcg Ala	caa Gln	ctg Leu	gtt Val	tca Ser	tcg Ser	tcc Ser	agc Ser	gac Asp	ctt Leu	tcg Ser	gcc Ala	816
260			265			270										
atc Ile	tgt Cys	gct Ala	cag Gln	gct Ala	cag Gln	att Ile	gat Asp	gtc Val	gag Glu	tgc Cys	cag Gln	aag Lys	ctt Leu	tcg Ser	gtc Val	864
275			280			285										
gcc Ala	cag Gln	gtc Val	tct Ser	acc Thr	gcc Ala	gtg Val	aac Asn	gag Glu	ttg Leu	gtt Val	gaa Glu	acc Thr	gtc Val	cag Gln	gca Ala	912
290			295			300										
ata Ile	gca Ala	aaa Lys	agc Ser	acc Thr	gaa Glu	gag Glu	gca Ala	gca Ala	aca Thr	gtc Val	gcc Ala	gtc Val	ttg Leu	gcc Ala	gat Asp	960
305			310			315			320							
gaa Glu	aag Lys	gca Ala	cgc Arg	ggg Gly	ggg Gly	gaa Glu	agt Ser	gtc Val	gtt Val	aac Asn	aag Lys	gcc Ala	gtt Val	gat Asp	ttc Phe	1008
325				330				335								
att Ile	gag Glu	cac His	ctc Leu	tcc Ser	gga Gly	gat Asp	atg Met	gcg Ala	gaa Glu	ctg Leu	gga Gly	gac Asp	gca Ala	atg Met	gag Glu	1056
340			345			350										



cgg Arg	ctt Leu	cag Gln	aac Asn	gac Asp	agt Ser	gcg Ala	cag Gln	atc Ile	aat Asn	aag Lys	gta Val	gta Val	gac Asp	gtc Val	att Ile	1104
		355				360						365				
aag Lys	gct Ala	gtg Val	gcg Ala	gag Glu	cag Gln	acc Thr	aat Asn	ctg Leu	cta Leu	gcc Ala	ctg Leu	aat Asn	gcg Ala	gcg Ala	ata Ile	1152
		370				375				380						
gag Glu	gcg Ala	gcc Ala	cgt Arg	gca Ala	gga Gly	gag Glu	cag Gln	ggc Gly	agg Arg	ggc Gly	ttt Phe	gcg Ala	gtc Val	gtg Val	gcg Ala	1200
		385				390				395				400		
gat Asp	gag Glu	gtt Val	cgt Arg	gct Ala	ttg Leu	gcg Ala	atg Met	cgc Arg	acc Thr	caa Gln	caa Gln	tcg Ser	acc Thr	aaa Lys	gaa Glu	1248
				405				410						415		
att Ile	gag Glu	agg Arg	cta Leu	gtg Val	gtt Val	tca Ser	ttg Leu	cag Gln	cag Gln	gga Gly	agt Ser	gaa Glu	gct Ala	gcg Ala	ggc Gly	1296
		420						425				430				
gag Glu	ttg Leu	atg Met	cgg Arg	cgt Arg	ggc Gly	aag Lys	gtc Val	cgg Arg	acg Thr	cat His	gac Asp	gtc Val	gtt Val	gga Gly	ttg Leu	1344
		435				440						445				
gcc Ala	cag Gln	caa Gln	gcc Ala	gcg Ala	cgc Arg	cgc Arg	gct Ala	act Thr	cga Arg	aat Asn	tac Tyr	cca Pro	gct Ala	gtc Val	gcc Ala	1392
		450				455				460						
ggc Gly	atc Ile	caa Gln	gcg Ala	atg Met	aac Asn	tat Tyr	cag Gln	atc Ile	gcc Ala	gct Ala	gga Gly	gca Ala	gag Glu	cag Gln	caa Gln	1440
		465				470				475				480		
ggg Gly	gct Ala	gct Ala	gtg Val	gtt Val	caa Gln	atc Ile	aac Asn	cag Gln	aat Asn	atg Met	ctt Leu	gaa Glu	gtg Val	cat His	aag Lys	1488
				485				490						495		
atg Met	gct Ala	gac Asp	gag Glu	tcc Ser	gcc Ala	att Ile	aaa Lys	gcg Ala	gga Gly	cag Gln	acc Thr	atg Met	aag Lys	tca Ser	tcg Ser	1536
		500						505				510				
aag Lys	gag Glu	ctt Leu	gct Ala	cac His	ctc Leu	ggc Gly	agt Ser	gcg Ala	cta Leu	caa Gln	aaa Lys	tcc Ser	gtt Val	gat Asp	cga Arg	1584
		515				520						525				
ttc Phe	cag Gln	ctg Leu	tag													1596
		530														

<210> 34

<212> PRT

<213> not required under old rule

Met Ile Ser Phe Ala Arg Met Ala Glu Ser Leu Gly Val Gln Ala Lys

5

10

15





gtccggcttg cagcgcacgc gcacagcaag gccgagcttc tcgagcttgt tcagcaaggg 240  
aaccagttgt ggtggttcga ttgcgagcat ccgcgctagg tcagcctgca taagcccagg 300  
gctcgcttcg atgattagaa gtgccgacag ctgcgccggg cgtaggatcat atggcgtcag 360  
ggcttcaatc aggccttgag cgagcttcag ctgtgagccg gcgtaaggca t 411

<210> 36  
<211> 136  
<212> PRT  
<213> not required under old rule

<400> 36  
Met Pro Tyr Ala Gly Ser Gln Leu Lys Leu Ala Gln Gly Leu Ile Glu  
1 5 10 15  
Ala Leu Thr Pro Tyr Asp Leu Arg Pro Ala Gln Leu Ser Ala Leu Leu  
20 25 30  
Ile Ile Glu Ala Ser Pro Gly Leu Met Gln Ala Asp Leu Ala Arg Met  
35 40 45  
Leu Ala Ile Glu Pro Pro Gln Leu Val Pro Leu Leu Asn Lys Leu Glu  
50 55 60  
Lys Leu Gly Leu Ala Val Arg Val Arg Cys Lys Pro Asp Lys Arg Ser  
65 70 75 80  
Tyr Gly Ile Phe Leu Ser Lys Ala Gly Glu Thr Gln Leu Lys Glu Leu  
85 90 95  
Lys Lys Ile Val Val Gln Ser Asp Gln Asp Ala Thr Ser Met Leu Ser  
100 105 110  
Asp Asp Glu Arg Glu Gln Leu Leu Leu Leu His Lys Ile His Ala  
115 120 125  
Glu Pro Glu Ala Gln Gln Leu Gly  
130 135

<210> 37  
<211> 1446  
<212> DNA  
<213> not required under old rule

<220>  
<221> CDS  
<222> (1)..(1443)  
<223> product = "Coniferylaldehyd-Dehydrogenase" / gene  
= "caldh"

[illegible]

99

aaa tcg ccg gtg atc gtt tcc cgc agt gca gat atg gcg gac gtt gca	720
Lys Ser Pro Val Ile Val Ser Arg Ser Ala Asp Met Ala Asp Val Ala	
225 230 235 240	
caa cgg gtg ttg acg gtg aaa acc ttc aat gcc ggg caa atc tgt ctg	768
Gln Arg Val Leu Thr Val Lys Thr Phe Asn Ala Gly Gln Ile Cys Leu	
245 250 255	
gca ccg gac tat gtg ctg ctg ccg gaa gaa tcg ctg gat agc ttt gtc	816
Ala Pro Asp Tyr Val Leu Leu Pro Glu Glu Ser Leu Asp Ser Phe Val	
260 265 270	
gcc gag gcg acg cgc ttc gtg gcc gca atg tat ccc tcg ctt cta gat	864
Ala Glu Ala Thr Arg Phe Val Ala Ala Met Tyr Pro Ser Leu Leu Asp	
275 280 285	
aat ccg gat tac acg tcg atc atc aat gcc cga aat ttc gac cgt ctg	912
Asn Pro Asp Tyr Thr Ser Ile Ile Asn Ala Arg Asn Phe Asp Arg Leu	
290 295 300	
cat cgc tac ctg act gat gcg cag gca aag gga ggg cgc gtc att gaa	960
His Arg Tyr Leu Thr Asp Ala Gln Ala Lys Gly Gly Arg Val Ile Glu	
305 310 315 320	
atc aat cct gcg gcc gaa gag ttg ggg gat agt ggt atc agg aag atc	1008
Ile Asn Pro Ala Ala Glu Glu Leu Gly Asp Ser Gly Ile Arg Lys Ile	
325 330 335	
gcg ccc act ttg atc gtg aat gtg tcg gat gaa atg ctg gtc ttg aac	1056
Ala Pro Thr Leu Ile Val Asn Val Ser Asp Glu Met Leu Val Leu Asn	
340 345 350	
gag gag atc ttt ggt ccg ctg ctc ccg atc aag act tat cgt gat ttc	1104
Glu Glu Ile Phe Gly Pro Leu Leu Pro Ile Lys Thr Tyr Arg Asp Phe	
355 360 365	
gac tcg gct atc gac tac gtc aac agc aag cag cga cca ctt gcc tcg	1152
Asp Ser Ala Ile Asp Tyr Val Asn Ser Lys Gln Arg Pro Leu Ala Ser	
370 375 380	
tac ttc ttc ggc gaa gat gcg gtt gag cgt gag caa gtg ctt aag cgt	1200
Tyr Phe Phe Gly Glu Asp Ala Val Glu Arg Glu Gln Val Leu Lys Arg	
385 390 395 400	
acg gtt tcg ggc gcc gtg gtc gtg aac gat gtc atg agc cat gtg atg	1248
Thr Val Ser Gly Ala Val Val Val Asn Asp Val Met Ser His Val Met	
405 410 415	
atg gat acg ctt cca ttt ggt ggt gtg ggg cac tcg ggg atg ggg gca	1296
Met Asp Thr Leu Pro Phe Gly Gly Val Gly His Ser Gly Met Gly Ala	
420 425 430	
tat cac ggc att tat ggt ttc cga acc ttc agc cat gcc aag cct gtt	1344
Tyr His Gly Ile Tyr Gly Phe Arg Thr Phe Ser His Ala Lys Pro Val	
435 440 445	







<210> 39  
 <211> 1827  
 <212> DNA  
 <213> not required under old rule

<400> 39  
 ctatttgtct agtggtcggc gcgaaattcg ataagaaagc tgggcgag tgaggccgag 60  
 ccggcgggca gttccgaga cattgccttt cacctggccc agagcatggc taatcatcgc 120  
 gtcctccact tcttgacgag tcacgcgcgt caggctccttt gaggcaagcg gcgagtcgat 180  
 tgtgctggtc ggtttgaga aggaagtact tgggctgcca gtttctgtg gctgattatc 240  
 ttgagcggtg gccaggatgc cgctggcccc aatggagaac atcggttgag tcagtcgttc 300  
 accgctagtg aagagggtggc tcacgtcaat ggctccatcc tccggagcgc tgatgactcc 360  
 gcgctccacc aaattttgaa gctcccgat gtttctgga aagtcgtagc caagcagggc 420  
 attggctgca cgtggagtga atccgctgac caccggcta tgacgctgat tgaagcggtg 480  
 caggaaatag gtcacagga ggggaatgtc ttccttctc tctcgaagcg gcgggaggtg 540  
 gatcgggtaa acattgaggc ggaaaaaag gtcctcgagg aactcgccgc gctggacgcc 600  
 tgccggaaga tcgacattgg ttgcggctac cacacggagc tcaaccttga gtgtcctgct 660  
 tccgccaacc cgttcgacct ccgactcttg cagggcgga agtaacttcc cttggggccac 720  
 gaggcttagc gtccctatct cgtcaaggaa tagtgtgccc cccgaagcgc gctcgaaccg 780  
 tctgtctga gattgggtgg cgccggtaaa cccccccgt tcgacgccga acaactcgga 840  
 ctccatcagg gtttcgggaa tacgtgcgca attgaccgca acaaacgggc cgtcgtgtct 900  
 ggggctgatg cggggaagca tgcgggcgaa catctccttg ccacacactg attcaccgct 960  
 aaacagtacc gtcgcctccg tgggtgctac gcgcttcagc atgtggcagg cagcattgaa 1020  
 tgccgaggaa attcccacca tgcgtgttc cgatgcagtg cttgagtctg cggcggagtg 1080  
 atggggagtg ttcctttgtc cctgtgcgt tcttcgtctc tgcggcgtgc ttggttgccg 1140  
 acaaatggtt gcgctaagcg ccgccaagtc ctcttcggcg tcttccatt cttccgctgg 1200  
 cttgccgatc atgcggcaga tctgcgaacc cgtggagcgg cattccacct ctcggtaaag 1260  
 gatgaggcga ccaaccagcg cggacgtata gccaatggca taaccgctct gcgtccagca 1320  
 cgcgggctcg gtgccgatgc cgtagtgcgc aatatgttca tcatcttcgc tcgaatggtg 1380  
 ccagaggaat tcgccgtagt aggtcccaa atccatgtcg aagtcgaagt ggatcggctc 1440  
 cacgcgtact gcgccttcca gagagtgcaa gttcgggccc gcggcaaata gggagagcgg 1500  
 atcggcgctt ctgaagcgt ccttcagaag ggcgcatct ttggcgccgc agtggttaacc 1560

003221-92605450

ggttcgcagc atgattccgc gggcgcgggc gaagcccacg ctttcaatta attcgcgtcg 1620  
caatgcaccc agtccgctgc tgtggaggag cagcattcgc gcgccgttca accagatgcg 1680  
tccatcgcca gggctgaaaa ggagggattc agtgaggtca tgaagggagg ggacggcgcc 1740  
tggctccaat tgctcgatgg cgccgcgatt gagtgtcttg ggcgcggtct tggagagttc 1800  
ggctagggag ataaatttgc tggccat 1827

<210> 40  
<211> 608  
<212> PRT  
<213> not required under old rule

<400> 40  
Met Ala Ser Lys Phe Ile Ser Leu Ala Glu Leu Ser Lys Thr Ala Pro  
1 5 10 15  
Lys Thr Leu Asn Arg Gly Ala Ile Glu Gln Leu Glu Pro Gly Ala Val  
20 25 30  
Pro Ser Leu His Asp Leu Thr Glu Ser Leu Leu Phe Ser Pro Gly Asp  
35 40 45  
Gly Arg Ile Trp Leu Asn Gly Ala Arg Met Leu Leu Leu His Ser Ser  
50 55 60  
Gly Leu Gly Ala Leu Arg Arg Glu Leu Ile Glu Ser Val Gly Phe Ala  
65 70 75 80  
Arg Ala Arg Gly Ile Met Leu Arg Thr Gly Tyr His Cys Gly Ala Lys  
85 90 95  
Asp Ala Ala Leu Leu Lys Glu Arg Phe Ser Asn Ala Asp Pro Leu Ser  
100 105 110  
Leu Phe Ala Ala Gly Pro Asn Leu His Ser Leu Glu Gly Ala Val Arg  
115 120 125  
Val Glu Pro Ile His Phe Asp Phe Asp Met Asp Leu Gly Thr Tyr Tyr  
130 135 140  
Gly Glu Phe Leu Trp His His Ser Ser Glu Asp Asp Glu His Ile Ala  
145 150 155 160  
His Tyr Gly Ile Gly Thr Glu Pro Ala Cys Trp Thr Gln Thr Gly Tyr  
165 170 175  
Ala Ile Gly Tyr Thr Ser Ala Leu Val Gly Arg Leu Ile Leu Tyr Arg  
180 185 190  
Glu Val Glu Cys Arg Ser Thr Gly Ser Gln Ile Cys Arg Met Ile Gly  
195 200 205

Lys	Pro	Ala	Glu	Glu	Trp	Glu	Asp	Ala	Glu	Glu	Asp	Leu	Ala	Ala	Leu
210						215			220						
Ser	Ala	Thr	Ile	Cys	Arg	Gln	Pro	Ser	Thr	Pro	Gln	Arg	Arg	Arg	Thr
225			230						235			240			
Gln	Gln	Gly	Gln	Arg	Asn	Thr	Pro	His	His	Ser	Ala	Ala	Asp	Ser	Ser
			245						250			255			
Thr	Ala	Ser	Glu	His	Asp	Met	Val	Gly	Ile	Ser	Ser	Ala	Phe	Asn	Ala
			260			265						270			
Ala	Cys	His	Met	Leu	Lys	Arg	Val	Ala	Pro	Thr	Glu	Ala	Thr	Val	Leu
275						280			285						
Phe	Thr	Gly	Glu	Ser	Gly	Val	Gly	Lys	Glu	Met	Phe	Ala	Arg	Met	Leu
290			295						300						
His	Arg	Ile	Ser	Pro	Arg	His	Asp	Gly	Pro	Phe	Val	Ala	Val	Asn	Cys
305			310						315			320			
Ala	Arg	Ile	Pro	Glu	Thr	Leu	Met	Glu	Ser	Glu	Leu	Phe	Gly	Val	Glu
			325			330						335			
Arg	Gly	Ala	Phe	Thr	Gly	Ala	Thr	Gln	Ser	Arg	Ala	Gly	Arg	Phe	Glu
			340			345						350			
Arg	Ala	Ser	Gly	Gly	Thr	Leu	Phe	Leu	Asp	Glu	Ile	Gly	Thr	Leu	Ser
355						360			365						
Leu	Val	Ala	Gln	Gly	Lys	Leu	Leu	Arg	Ala	Leu	Gln	Glu	Ser	Glu	Val
370			375						380						
Glu	Arg	Val	Gly	Gly	Ser	Arg	Thr	Leu	Lys	Val	Asp	Val	Arg	Val	Val
385			390						395			400			
Ala	Ala	Thr	Asn	Val	Asp	Leu	Arg	Ala	Gly	Val	Gln	Arg	Gly	Glu	Phe
			405			410						415			
Arg	Glu	Asp	Leu	Phe	Phe	Arg	Leu	Asn	Val	Tyr	Pro	Ile	His	Leu	Pro
420						425			430						
Pro	Leu	Arg	Glu	Arg	Lys	Glu	Asp	Ile	Pro	Leu	Leu	Met	Thr	Tyr	Phe
435			440						445						
Leu	His	Arg	Phe	Asn	Gln	Arg	His	Ser	Arg	Val	Val	Ser	Gly	Phe	Thr
450			455						460						
Pro	Arg	Ala	Ala	Asn	Ala	Leu	Leu	Gly	Tyr	Asp	Phe	Pro	Gly	Asn	Ile
465			470						475			480			
Arg	Glu	Leu	Gln	Asn	Leu	Val	Glu	Arg	Gly	Val	Ile	Ser	Ala	Pro	Glu
			485			490						495			
Asp	Gly	Ala	Ile	Asp	Val	Ser	His	Leu	Phe	Thr	Ser	Gly	Glu	Arg	Leu
			500			505						510			

Thr Gln Pro Met Phe Ser Ile Gly Ala Ser Gly Ile Leu Ala Thr Ala  
515 520 525

Gln Asp Asn Gln Pro Gln Glu Thr Gly Ser Pro Ser Thr Ser Phe Ser  
530 535 540

Lys Pro Thr Ser Thr Ile Asp Ser Pro Leu Asp Ser Lys Asp Leu Ser  
545 550 555 560

Ala Met Thr Leu Gln Glu Val Glu Asp Ala Met Ile Ser His Ala Leu  
565 570 575

Gly Gln Val Lys Gly Asn Val Ser Glu Ala Ala Arg Arg Leu Gly Leu  
580 585 590

Thr Arg Ala Gln Leu Ser Tyr Arg Ile Ser Arg Arg Pro Leu Asp Lys  
595 600 605

<210> 41  
<211> 768  
<212> DNA  
<213> not required under old rule

<220>  
<221> CDS  
<222> (1)..(765)  
<223> product = "Coniferylalkohol-Dehydrogenase" / gene  
= "cadh"

<400> 41  
atg caa ctg acc aac aag aaa atc gtc gtc acc gga gtg tcc tcc ggt 48  
Met Gln Leu Thr Asn Lys Lys Ile Val Val Thr Gly Val Ser Ser Gly  
1 5 10 15

atc ggt gcc gaa act gcc cgc gtt ctg cgc tct cac ggc gcc aca gtg 96  
Ile Gly Ala Glu Thr Ala Arg Val Leu Arg Ser His Gly Ala Thr Val  
20 25 30

att ggc gta gat cgc aac atg ccg agc ctg act ctg gat gct ttc gtt 144  
Ile Gly Val Asp Arg Asn Met Pro Ser Leu Thr Leu Asp Ala Phe Val  
35 40 45

cag gct gac ctg agc cat cct gaa ggc atc gat aag gcc atc tct cag 192  
Gln Ala Asp Leu Ser His Pro Glu Gly Ile Asp Lys Ala Ile Ser Gln  
50 55 60

ctg ccg gag aaa att gac gga ctc tgc aat atc gcc ggg gtg ccc ggc 240  
Leu Pro Glu Lys Ile Asp Gly Leu Cys Asn Ile Ala Gly Val Pro Gly  
65 70 75 80

act gcc gat cct cag ctc gtc gca aac gtg aac tac ctg ggt cta aag 288  
Thr Ala Asp Pro Gln Leu Val Ala Asn Val Asn Tyr Leu Gly Leu Lys  
85 90 95

tat	ctg	acc	gag	gca	gtc	ctg	tcg	cgc	att	caa	ccc	ggg	ggg	tcg	att	336
Tyr	Leu	Thr	Glu	Ala	Val	Leu	Ser	Arg	Ile	Gln	Pro	Gly	Gly	Ser	Ile	
			100					105					110			
gtc	aac	gtg	tcc	tct	gtg	ctt	ggc	gcc	gag	tgg	ccg	gcc	cgc	ctt	cag	384
Val	Asn	Val	Ser	Ser	Val	Leu	Gly	Ala	Glu	Trp	Pro	Ala	Arg	Leu	Gln	
		115					120					125				
ttg	cat	aag	gag	ctg	ggg	agt	gtt	gtt	gga	ttc	tcc	gaa	ggc	cag	gca	432
Leu	His	Lys	Glu	Leu	Gly	Ser	Val	Val	Gly	Phe	Ser	Glu	Gly	Gln	Ala	
	130					135				140						
tgg	ctt	aag	cag	aat	cca	gtg	gcc	ccc	gaa	ttc	tgc	tac	cag	tat	ttc	480
Trp	Leu	Lys	Gln	Asn	Pro	Val	Ala	Pro	Glu	Phe	Cys	Tyr	Gln	Tyr	Phe	
145				150					155						160	
aaa	gaa	gca	ctg	atc	gtt	tgg	tct	caa	gtt	cag	gcg	cag	gaa	tgg	ttc	528
Lys	Glu	Ala	Leu	Ile	Val	Trp	Ser	Gln	Val	Gln	Ala	Gln	Glu	Trp	Phe	
			165					170					175			
atg	agg	acg	tct	gta	cgc	atg	aac	tgc	atc	gcc	ccc	ggc	cct	gta	ttc	576
Met	Arg	Thr	Ser	Val	Arg	Met	Asn	Cys	Ile	Ala	Pro	Gly	Pro	Val	Phe	
		180						185					190			
act	ccc	att	ctc	aat	gag	ttc	gtc	acc	atg	ctg	ggg	caa	gag	cgg	act	624
Thr	Pro	Ile	Leu	Asn	Glu	Phe	Val	Thr	Met	Leu	Gly	Gln	Glu	Arg	Thr	
		195					200					205				
cag	gcg	gac	gct	cat	cgt	att	aag	cgc	cca	gca	tat	gcc	gat	gaa	gtg	672
Gln	Ala	Asp	Ala	His	Arg	Ile	Lys	Arg	Pro	Ala	Tyr	Ala	Asp	Glu	Val	
	210					215				220						
gcc	gcg	gtg	att	gca	ttc	atg	tgt	gct	gag	gag	tca	cgt	tgg	atc	aac	720
Ala	Ala	Val	Ile	Ala	Phe	Met	Cys	Ala	Glu	Glu	Ser	Arg	Trp	Ile	Asn	
225				230					235					240		
ggc	ata	aat	att	cca	gtg	gac	gga	ggg	ttg	gca	tcg	acc	tac	gtg	taa	768
Gly	Ile	Asn	Ile	Pro	Val	Asp	Gly	Gly	Leu	Ala	Ser	Thr	Tyr	Val		
			245					250					255			

<210> 42

<211> 255

<212> PRT

<213> not required under old rule

<400> 42

Met	Gln	Leu	Thr	Asn	Lys	Lys	Ile	Val	Val	Thr	Gly	Val	Ser	Ser	Gly
1				5				10					15		

Ile	Gly	Ala	Glu	Thr	Ala	Arg	Val	Leu	Arg	Ser	His	Gly	Ala	Thr	Val
		20					25					30			

Ile	Gly	Val	Asp	Arg	Asn	Met	Pro	Ser	Leu	Thr	Leu	Asp	Ala	Phe	Val
		35					40					45			



<222> (12)

<220>

<221> UNSURE

<222> (13)..(19)

<400> 44

Met Gln Leu Thr Asn Lys Lys Ile Val Val Val Xaa Val Xaa Xaa Xaa  
1 5 10 15

Xaa Xaa Xaa Xaa  
20

<210> 45

<211> 20

<212> PRT

<213> not required under old rule

<220>

<221> UNSURE

<222> (20)

<400> 45

Ser Ile Leu Gly Leu Asn Gly Ala Pro Val Gly Ala Glu Gln Leu Gly  
1 5 10 15

Ser Ala Leu Xaa  
20